09/743825

FILE 'REGISTRY' ENTERED AT 15:58:21 ON 12 AUG 2005
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STRUCTURE FILE UPDATES: 11 AUG 2005 HIGHEST RN 859751-76-1 DICTIONARY FILE UPDATES: 11 AUG 2005 HIGHEST RN 859751-76-1

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TSCA INFORMATION NOW CURRENT THROUGH JANUARY 18, 2005

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Structure search iteration limits have been increased. See HELP SLIMITS for details.

Experimental and calculated property data are now available. For more information enter HELP PROP at an arrow prompt in the file or refer to the file summary sheet on the web at: http://www.cas.org/ONLINE/DBSS/registryss.html

0 GCATGTTACAGGTAGAAAAGCC/SQEP

123660 SOL=22

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0 GCATGTTACAGGTAGAAAAGCC/SQEP
 (GCATGTTACAGGTAGAAAAGCC/SQEP AND SQL=22)

O CTGGCGTATCTGAAGAGTCTG/SQEP

335042 SQL=21

0 CTGGCGTATCTGAAGAGTCTG/SQEP (CTGGCGTATCTGAAGAGTCTG/SQEP AND SQL=21)

O GACCGCATAGACTTCTCAGA/SQEP

452450 SQL=20

0 GACCGCATAGACTTCTCAGA/SQEP (GACCGCATAGACTTCTCAGA/SQEP AND SQL=20)

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FILE 'HOME' ENTERED AT 15:58:30 ON 12 AUG 2005

FILE REGISTRY

Property values tagged with IC are from the ZIC/VINITI data file provided by InfoChem.

STRUCTURE FILE UPDATES: 11 AUG 2005 HIGHEST RN 859751-76-1 DICTIONARY FILE UPDATES: 11 AUG 2005 HIGHEST RN 859751-76-1

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TSCA INFORMATION NOW CURRENT THROUGH JANUARY 18, 2005

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* The CA roles and document type information have been removed from the IDE default display format and the ED field has been added, the effective March 20, 2005. A new display format, IDERL, is now the available and contains the CA role and document type information.

Structure search iteration limits have been increased. See HELP SLIMI for details.

Experimental and calculated property data are now available. For more information enter HELP PROP at an arrow prompt in the file or refer to the file summary sheet on the web at: http://www.cas.org/ONLINE/DBSS/registryss.html

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Patent: JP 2001169787-A 43 26-JUN-2001;

PFIZER PRODUCTS INC

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(bases 1 to 20)

Griffais,R., Hoiseth,S.K., Zagursky,R.J., Metcalf,B.J., Peek,J.A., Sankaran,B. and Fletcher,L.D.
Chlamydia pneumoniae polynucleotides and uses thereof Patent: US 6559294-A 5333 06-MAY-2003;
143991 Sequence 9
AK493229 Sequence
AX010205 Sequence
AX405000 Sequence
AX412214 Sequence
AX61528 Sequence
AX61558 Sequence
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PAT 04-OCT-2004

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Unclassified.

1 (bases 1 to 18)

Tsarev,S.A., Emerson,S.U. and Purcell,R.H.
Recombinant proteins of a Pakistani strain of hepatitis E and their
use in diagnostic methods and vaccines
Patent: US 6207416-A 53 27-MAR-2001;
Method for the preparation of selectively randomised nucleic acid molecules Patent: WO 0222634-A 25 21-MAR-2002; Sangamo Blosciences Inc. (US) Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cobleigh, M.A., Shak, S., Baker, J.B. and Cronin, M.T.
Gene expression markers for breast cancer prognosis
Patent: WO 2004065583-A 191 05-AUG-2004;
Genomic Health, Inc. (US); Rush University Medical Center (US)
Location/Qualifiers
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                                                                                                                                                                                                                        58.2%; Score 12.8; DB 6; 61.1%; Pred. No. 2.1e+05; tive 5; Mismatches 2;
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="texon:32630"
/note="reverse primer"
                                                                                                               /organism="synthetic construct"
                                                                                                                                                                                                                                                                                                                                                                                                                             CQ876341 21 bp DNA Sequence 191 from Patent WO2004065583.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           other sequences; artificial sequences.
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Sequence 53 from patent US 6207416.
AR138875.1 GI:14482371
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/organism="unknown"
/mol_type="unassigned DNA"
                                                                                                                              /mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Oligonucleotide"
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Best Local Similarity 61.19
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Bukaryota; Butheria; Primates; Catarrhini; Hominidae; Homo.

But (bases 1 to 19)

Tavtigian, S.V., Teng. D.H.F., Simard, J. and Rommens, J.M.
Chromosome 17q-linked prostate cancer susceptibility gene
Datent: JP 200559065-A 156 10-SEP-2002;
MYRIAD GENETICS INC, THE HOSPITAL FOR SICK CHILDREN
OS Homo sapiens (human)
PN JP 2002529065-A/156
PD 10-SEP-2002
PP 05-NOV-1999 UP 2000581041
PR 06-NOV-1999 US 60/107468
PP SEAN V TAVTIGIAN, DAVID H F TENG, JACQUES SIMARD, JOHANNA M PI
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PC A61P35/00,
PC C07K14/47,C07K16/18,C07K16/44,C12N1/15,C12N1/19,C12N1/21,C12NS/ PC
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GGIN37/00,C12N15/00,A61K37/02,C12N5/00
Chromosome 17q-linked prostate cancer susceptibility gene
Location/Qualifiers
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                      60.0%; Score 13.2; DB 6; Length 21; 83.3%; Pred. No. 1.3e+05; ive 0; Mismatches 3; Indels
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Sequence 25 from Patent W00222634.
AX405008
AX405008.1 GI:21438223
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Homo sapiens (human)
Homo sapiens
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synthetic construct
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ses 14; Conservative
                                            Local Similarity 83.3
nes 15; Conservative
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AX405008/c
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BD231604/c
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PAT 16-JUN-2001

REFERENCE AUTHORS

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PAT 14-MAY-2004

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Tobases 1 to 18)

Tsarev, S.A., Emerson, S.U. and Purcell, R.H.
Recombinant proteins of a pakistani strain of hepatitis E and their use in diagnostic methods and vaccines
Patent: US 6708873-A 53 16-MAR-2004;
Location/Qualifiers
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Cohen, D., Chumakov, I. and Blumenfeld, M.
Biallelic markers for use in constructing a high density
disequilibrium map of the human genome
Patent: US 637751-A 4779 25-MAR-2003;
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55.5%; Score 12.2; DB 6; 82.4%; Pred. No. 4.2e+05; artive 0; Mismatches 3;
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Sequence 4779 from patent US 6537751.
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/organism="unknown"
/mol_type="genomic DNA"
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/wol_type="genomic DNA"
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                                                   AR293044.1 GI:31680328
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1 (Dases I to 18)

1 (Dases I to 20)

Tarrev, S.A., Emerson, S.U. and Purcell, R.H.
Recombinant proteins of a Pakistani strain of hepatitis E and their use in diagnostic methods and vaccines
Patent: US 6287759-A 53 11-SEP-2001;
Location/Qualifiers
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Emerson, S.U., Purcell, R.H., Tsarev, S.A. and Robinson, R.A.
Recombinant proteins of a Pakistani strain of hepatitis E and their
use in diagnostic methods and vaccines
Patent: US 6458562-A 53 01-007-2002;
Location/Qualifiers
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0; Mismatches 3; Indels
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                             55.5%; Score 12.2; DB 6; 82.4%; Pred. No. 4.2e+05; ive 0; Mismatches 3;
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AR234243
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Sequence 53 from patent US 6287759.
AR167519
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/wol_type="genomic DNA"
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/organism="unknown"
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82.4%;
                           Query Match 55.5
Best Local Similarity 82.4
Matches 14; Conservative
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DEFINITION ACCESSION VERSION

RESULT 10 AR234243

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/note="upstream amplification primer 99-44259 for SEQ 103"

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                1 (bases 1 to 20)
Bennett, C. Frank. and Cowsert, L.M.
Antisense modulation of talin expression
Patent: US 6372492-A 44 16-APR-2002;
Location/Qualifiers
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Patent: US 6503152-A 50 07-JAN-2003;
Location/Qualifiers
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Sequence 274 from Patent WO0206525.
AX378485
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/db_xref="taxon:9606"
1. .21
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Sequence 50 from patent US 6503152.
AR271107
                                                                                                                                           /organism="unknown"
/mol_type="unassigned DNA"
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Best Local Similarity 82.4
Matches 14; Conservative
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Recombinant proteins of a pakistani strain of hepatitis E and their use in diagnostic methods and vaccines
Patent: JP 2001524821-A 50 04-DEC-2001;
THE GOVERNENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY SECRETARY DEPARTMENT OF HEALTH AND HUMAN SERVICES
                                                                                                                                                                                                                                                                                   BD084547 17-AUG-2002 Recombinant proteins of a pakistani strain of hepatitis E and their use in diagnostic methods and vaccines.
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CC Topology: Linear;

CC Recombinant proteins of a pakistani strain of hepatitis E and their use in their use in Location/Qualifiers

CC diagnostic methods and vaccines

FH Key Location/Qualifiers

FT source | 1.18

/organism='Unidentified'.
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JP 2001524821-A/50
04-DEC-2001
09-PR-1990 UP 1998544174
11-APR-1997 US 08/840316
SUZANNE U EMERSON, ROBERT H PURCELL, SERGEI A TSAREV, ROBIN A
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                                                                                      Query Match 55.5%; Score 12.2; DB 6; Length 18; Best Local Similarity 82.4%; Pred. No. 4.2e+05; Matches 14; Conservative 0; Mismatches 3; Indels
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Sequence 44 from patent US 6372492.
AR207150
AR207150.1 GI:21505970

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JP 2001524821-A/50.
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AR207150/c
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RESULT 19 CQ763548/c

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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                       1 (bases 1 to 20)
Cohen,D., Chumakov.I. and Blumenfeld,M.
Bialleller markers for use in constructing a high density disequilibrium map of the human genome Patent: US 6537751-A 9693 25-MAR-2003;
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synthetic construct
other sequences; artificial sequences.
         20 bp DNi
Sequence 9693 from patent US 6537751.
AR297958
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Patent: WO 0222634-A 19 21-MAR-2002;
Sangamo Biosciences Inc. (US)
Location/Qualifiers
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Sequence 19 from Patent WO0222634.
AX405002
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                                                                   AR297958.1 GI:31685242
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Best Local Similarity 66.7<sup>3</sup>
Matches 12, Conservative
                                                                                                                        Unknown.
Unclassified.
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Uchida,K., Uchida,T., Tanaka,Y., Matsuda,Y. and Kondo,S.
Antisense nucleic acid compound targeted to VEGF
Patent: US 6150092-A 23 21-NOV-2000;
Location/Qualifiers
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                                  55.5%; Score 12.2; DB 6; Length 21; 82.4%; Pred. No. 4.2e+05; ive 0; Mismatches 3; Indels
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                                                                                                                                                                                                                                 linear
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Patent: WO 2004003201-A 2166 08-JAN-2004;
Pharmacia Corporation (US)
Location/Qualifiers
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db xref="texon.32630"
/note="Human LRH1 antisense"
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Sequence 2166 from Patent WO2004003201.
CQ763548 GI:44906784
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/organism="unknown"
/mol_type="unassigned DNA"
                                                                                                                                                                                                                           Sequence 23 from patent US 6150092. AR118897
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1 GCATGGTGGAGGTAGAGCAG 20
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Matches 14; Conserv
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PAT 14-JUN-2002

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1 (bases 1 to 19)
Cohen, D., Chumakov, I. and Blumenfeld, M.
Biallelic markers for use in constructing a high density
                                                                                                                                                                                                                                  Length 17;
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Synthetic P.falciparum 155 gene PCR primer RIT34.
A33496
                                                                                                                                                                                                                                                                                                                                                                                                           linear
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             24-APR-2001
20-NOV-1997 JP 1998523766
20-NOV-1996 US 08/752919
20FFFREY BONADIO,JIANMING FANG
CO7121/04,CI2N15/00,CI2NS/16
Synthetic oligonucleotide
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86.7%; Pred. No. 6.8e+05;
tive 0; Mismatches 2;
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    1. 17
    forganism="synthetic construct"
/mol type="genomic DNA"
    /db_xref="taxon:32630"

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Pred. No. 6.8e+05;
0; Mismatches 2
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1 (bases 1 to 20)
Holmes, M.J. and Uhlen, M.
Solid Phase Diagnosis of MEDICAL CONDI
Patent: WO 9011369-A 21 04-OCT-1990;
CEMU BIOTEKNIK (SE)

    .20
    /organism="synthetic const:
/mol_type="unassigned DNA"

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/mol_type="genomic DNA"
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JP 2001505420-A/14
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Best Local Similarity 86.77
Matches 13, Conservative
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Nucleotide and protein sequences of liver activin/inhibin and
methods based thereon.
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                Robbins,J.M. and Tritz,R.
Ribozyme therapy for the treatment of proliferative skin and eye disease.

Ribozyme therapy for the treatment of proliferative skin and eye patent: WO 0130362-A 4514 03-MAY-2001;

IMMUSOL, INC. (US)
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Patent: WO 2004063366-A. 9 29-JUL-2004;
BASF AKTIENCESELLSCHAFT (DE)
Location/Qualifiers
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1 (bases 1 to 17)

Bonadio,J. and Pang,J.

Wucleotide and protein sequences of liver activin/inhibin and methods based thereon
Patent: JP 201505420-A 14 24-APR-2001;

THE REGENTS OF THE UNIVERSITY OF MICHIGAN

S Artificial Sequence
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                                                                                                                                        /mol_type="unassigned DNA"
/db_xref="taxon:9606"
/noTe="VBGF hammerhead ribozyme recognition site"
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Pred. No. 5.3e+05;
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
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Sequence 9 from Patent WO2004063366.

    .21
    /organism="Homo sapiens"

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Location/Qualifiers
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JP 2001505420-A/14.
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Matches 15; Conservative 0
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PAT 23-AUG-2004
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                                                                                                                                Choo, Y. and Isalan, M. Method for the preparation of selectively randomised nucleic acid
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/db_xref="taxon:32610"
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/db_xref="caxon:32630"
/note="Oligonucleotide"
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Patent: WO 0222634-A 23 21-MAR-2002;
Sangamo Biosciences Inc. (US)
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Sangamo Biosciences Inc. (US)
Location/Qualifiers
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Sequence 27 from Patent WO0222634.
Sequence 23 from Patent WO0222634.
AX405006
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AX405010.1 GI:21438225
                                         AX405006.1 GI:21438221
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18 SYKCGAGKYAGAAAGC 2
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Best Local Similarity 58.89
Matches 10; Conservative
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CQ854109/c
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                                                           Length 20;
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Pred. No. 6.8e+05;
0; Mismatches 2; Indels
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                                                                                       2; Indels
                                                                                                                                                                                                                                                                                                                             Unclassified.

1 (bases 1 to 20)
Zhang,H. and Cowsert,L.M.
Antisense modulation of caspase 8 expression
Patent: US 6258600-A 98 10-JUL-2001;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Uhlen, M.
Solid phase diagnosis of medical conditions
Patent: US 5629158-A 27 13-MAY-1997;
                                                       Score 11.8; DB 6;
Pred. No. 6.8e+05;
0; Mismatches 2;
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/organism="unknown"
/mol_type="unassigned DNA"
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Sequence 27 from patent US 5629158.
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             /db_xref="taxon:32630"
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86.7%;
                                                         53.6%;
86.7%;
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1 (bases 1 to 20)
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Best Local Similarity 86.7
Matches 13; Conservative
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Matches 13
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AX405006/c
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ORGANISM

RESULT 28

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I42395/c

REFERENCE AUTHORS

TITLE JOURNAL FEATURES

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TITLE JOURNAL FEATURES

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AB068139 22 bp DNA linear SYN 21-MAY-2003
Synthetic construct DNA, reverse primer for human STS
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JP 2001321190-A/1822
20-NOV-2001
12-MAR-2001 JP 2001068285
EIICHI SOEDA
CI2N15/09,CI2N15/09,CI2N1/00,CI2Q1/68,G01N33/53,G01N33/566,
12-MAR-2001 JP 2001068285
EIICHI SOEDA
C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N33/53,G01N33/566,
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synthetic construct
of the sequences artificial sequences.
1 (bases 1 to 22)
Soeda, B.
Amethd of arraying genome clone
Patent: JP 2001231190-A 1822 20-NOV-2001;
THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH, YUGENKAISHA
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                                                                                                                  /organism='Artificial Sequence'
Location/Qualifiers
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                                                                         Description of Artificial Sequence:Synthetic
Location/Qualifiers
source 1. .22
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86.7%; Pred. No. 6.7e+05;
iive 0; Mismatches 2;
                                                                                                                                                                                                                                             DB 6;
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
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/organism="synthetic construct"
/mol_type="genomic.DNA"
/db_xref="taxon:32630"
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A method of arraying genome clone.
BD089578
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Best Local Similarity
Matches 13; Conserv
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AB068139
LOCUS
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TITLE
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Patent: JP 2001321190-A 1660 20-NOV-2001;
THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH, YUGENKAISHA
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Compositions against cancer antigen liv-1 and uses thereof
Patent: WO 2004067564-A 12 - AUG-2004;
PROTEIN DESIGN LABS, INC. (US)
Location/Qualifiers
                 Law,D., Gish,K.C., Murray,R. and Culp,P. Compositions against cancer antigen liv-1 and uses thereof Patent: WO 2004067564-A 11 12-AUG-2004; PROTEIN DESIGN LABS, INC. (US)
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86.7%; Pred. No. 6.7e+05;
iive 0; Mismatches 2;
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86.7%; Pred. No. 6.7e+05;
tive 0; Mismatches 2;
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/mol_type="unassigned DNA"
/mole="BCR4-53 sense siRNA"
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Sequence 12 from Patent WO2004067564.
CQ854110
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1 (bases 1 to 22)
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A method of arraying genome c
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JP 2001321190-A/1660
20-NOV-2001
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JP 2001321190-A/1660.
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Best Local Similarity 86.7
Matches 13; Conservative
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CQ854110
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/organism="synthetic construct"
/mol type="unassigned DNA"
/bb xref="taxon:32630"
/noFe="Human LRH1 antisense"
Tel:81-22-717-8042, Fax:81-22-717-8047)
Location/Qualifiers
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/mol_type="genomic DNA"
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                                                                                                                                            Chen, Y. Z., Hayashi, Y., Wu, J. G., Takaoka, E., Maekawa, K., Watanabe, N., Inazawa, J., Hosoda, F., Arai, Y., Mizushima, H., Morohashi, A., Ohira, M., Nakagawara, A., Liu, S., Hoshi, M., Horii, A. and Soeda, E.

A BAC-based STS-content map spanning a 35-Mb region of human chromosome 1p35-p36
Genomics 74 (1), 55-70 (2001)
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Genomics 74 (1), 55-70 (2001)
                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (04-AUG-2001) Akira Horii, Tohoku University School of Submitted (04-AUG-2001) Akira Horii, Tohoku University School of Medicine, Molecular Pathology; 2-1 Seiryomachi, Aoba-ku, Sendai, Miyagi 980-8575, Japan (E-mail:horii@mail.cc.tohoku.ac.jp, Tel:81-22-717-8047)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (04-AUG-2001) Akira Horii, Tohoku University School of Medicine, Molecular Pathology; 2-1 Seiryomachi, Aoba-ku, Sendai, Miyagi 980-8575, Japan (E-mail:horii@mail.cc.tohoku.ac.jp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="synthetic construct"
/mol_type="genomic DNA"
/do_Xrefe="taxon:32630"
/do_Xrefe="taxon:32630"
/do_ve="teverse primer for human STS sts-stGDB443043 at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TES-ELGDB443043 obtained from clones B58A11, B239M20, B215H8, B239P22, B239P22, B88A11, Human BAC library RPCI-11"
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                                                                      synthetic construct
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other sequences; artificial sequences.
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 sts-stGDB443043 at 1p36
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AB068139.1 GI:15128943
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AB068145.1 GI:15128949
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                                                                           /note="reverse primer for human STS sts-A002035 at 1p36 sts-A002035 obtained from clones B262K21, B239M20, B215H8, B239P22, B339P22, B301016, B262K21, Human BAC library RPCI-11"
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Cohen,D., Chumakov,I. and Blumenfeld,M.
Biallelic markers for use in constructing a high density disequilbrium map of the human genome Patent: US 6537751-A 4544 25-MAR-2003;
Location/Qualifiers
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86.7%; Pred. No. 6.7e+05;
tive 0; Mismatches 2;
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Patent: WO 2004003201-A 1397 08-JAN-2004;
Pharmacia Corporation (US)
Location/Qualifiers
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
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Sequence 1397 from Patent WO2004003201.
CQ762779
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AR292809
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Search completed: August 12, 2005, 09:25:09 Job time : 1571 secs
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1 (bases 1 to 20)

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PR 29-JUL-1999 JP 99P 248036,27-AUG-1999 JP 99P 300253 PR 29-JUL-1999 US 60/15950,17-FBR-2000 US 60/159590,17-FBR-2000 US 60/193322 PI TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAMA, KOJI HAYASHI, PI KAORU SAITO, PI JUNICHI YAMANOTO, SHIZUKO ISHII, TOMOYASU SUGIYAMA, AI WAKAMATSU, PI KEIICHI NAGAI, TETSUJI OTSUKI, KOJI MURAKAMI, KAZUHIRO YANO, PI
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                                                          52.7%; Score 11.6; DB 6;
77.8%; Pred. No. 8.6e+05;
Live 0; Mismatches 4;
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/organism="synthetic construct"
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Sequence 1730 from Patent WO2004003201.
CQ763112
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Description of Artificial Sequence:an artificially synthesized
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Best Local Similarity 77.8%; Pred. No. 8.6e+05;
Matches 14; Conservative 0; Mismatches 4;
                                                                                                                                    Location/Qualifiers

    .20
    /organism="synthetic construct"
|mol_type="genomic DNA"
|db_xref="taxon:32630"

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                                                                                            KOJI KANZAKI
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MAND SI JORA SIAII

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Aaq61732 HEV strai Aa27443 HEV strai Aav71653 HEV ORF p Aaz70423 Human bia AbB9241 Human Tal AdB90494 Human Tal AdG55754 Human TGF Adf90932 Microorga AbA86479 Human Oli Abd22709 Human my	Adp86599 Human Tal Aac73052 Single nu Abk41026 Human obe Adh56236 Yeast YFL Aac7537 Human bia Abk87660 Synthetic Adj17616 Antisense Adj101087 Human VEG Aah62090 VEGF hamm Ado16516 4 synthes Adq94527 Nostoc sp Aav38248 Murine li Aaz71716 Human bia Aaz71716 Human bia Aaz47049 Krg prime	Add15412 Mouse Cas Abk87664 Synthetic Add25041 Mouse cas Adj46478 Human PPP Adg15323 Human thy Adg15313 Human thy Adg15313 Human thy Adg15314 Human thy Adg15472 Human thy Adg8324 Human Chr Abra7279 BCR4-53 a Adr87260 BCR4-53 a Adr661778 Human Chr Adc39407 Novel hum Abc05087 TNFR1 exp Adr06117 Human TNF Adr06117 Human TNF Adr06117 Human Dia Abc11816 E Chaffee	Acc5549 Murine MI Abc291364 Homan oli Abc29362 Human oli Abc29364 Hose93-de Abc29364 Hose93-de Add577164 Acrisense Add577180 Antisense Adj16847 Antisense Adj16847 Antisense Adg77531 Canino di Abc71406 Oligonucl Abc71406 Oligonucl Abc71406 Oligonucl Abc71406 Oligonucl Abc71406 Oligonucl Abc71407 Oligonucl Abc71408 Human FAN Aad97256 Human EGF Aav97925 Human EGF Aav97922 Human EGF Aav97922 Human EGF Aav97922 Human EGF Aav97922 Human CFF Aav97924 Human Chr Aax61171 Human Chr Aax61171 Human Chr Aax61174 Human Chr Aax61174 Human Chr Aax61174 Human Chr Aax61174 Human Chr Aax61177 Human Obr Aax61174 Human Obr Aax61174 Human Obr
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Compugen Ltd. Compugen Ltd. Search time 239 Seconds without alignments) 44.913 Million cell updates/sec			the result being printed, re distribution. Description Aa25044 EST R0050 Aax5607 PCR prime Aa198006 Lawsonia Aca92364 Lawsonia Aca92364 Lawsonia Ad415895 Lawsonia Ad415845 Polymucle Aa465845 Polymucle Aa599071 Human pro Aa29301 Human pro Aa29301 PCR prime Ad46516 Synthetic Ad46516 Synthetic Ad46516 Transform Ad488282 Cancer de Ad50153 COX2 prob Ad413916 DMD regio Ad411032 Human HGP Ad411032 Human HGP
GenCore version 5.1.((c) 1993 - 2005 Compu, using sw model 2005, 04:53:41; Search search 544.91.	-09-743-825-7 gcatgttacaggtagaaaagcc 22 BNTITY NUC pop 10.0 , Gapext 1.0 90206 seqs, 2959870667 residues ts satisfying chosen parameters gth: 0	nimum Match 0% ximum Match 100% sting first 100 summaries Geneseq 16Dec04:* geneseqn1990s:* geneseqn2001s:* geneseqn2001as:* geneseqn2001as:* geneseqn2001as:* geneseqn2001as:* geneseqn2003bs:* geneseqn2003bs:* geneseqn2003bs:* geneseqn2003bs:* geneseqn2003ds:* geneseqn2003ds:* geneseqn2003ds:* geneseqn2003ds:* geneseqn2003ds:*	Equal to the score of the lysis of the total score of the

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Adg62530 Anti-inte
Aax88999 PCR prime
Aax88517 E. coll S
Aax38517 E. coll S
Aax24099 PCR prime
Aah37845 SNP speci
Aad35778 Human hIb
                                                                                                                                                                                                                                                                                                                        PB39; human; prostate cancer; PC; chromosome llpll.l-ll.2; cancer; coroctate epithellum; splicing mechanism; early diagnosis; progression; precancerous cell; metastatic potential; non-neoplastic prostate disease; expressed sequence tag; EST; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel gene which is dysregulated in prostate cancer useful for diagnosing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            method is selective and specific for various types of PC and also facilitates identifying prostate cancer of differing aggressiveness and metastatic potential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                ALIGNMENTS
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                            AAV84314
AAX38517
AAX94099
AAH37845
AAD35778
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                                                                                                                                                                                                         AAZ50444 standard; DNA; 22 BP.
                                                                                                                                                                                                                                                                                             EST R00504-specific primer 1.
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                                                                                                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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                4.4.4.4.4.
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                                                                                                                          Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis; sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine; neutralising epitope; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Htrh; Ponh; HypC; YefW; ABC1; Omp100; Lawsonia intracellularis infection; vaccine; PCR primer; probe; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lawsonia intracellularis protein related oligonucleotide SEQ ID NO: 50.
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                                                                                                      PCR primer used to amplify an ORF of Chlamydia pneumoniae.
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85.0%; Pred. No. 1.2e+03;
ive 0; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genome sequence of Chlamydia pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Page 1792; Disclosure; 1912pp; English
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98US-0107078P.
            AAX96007 standard; DNA; 20
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                                                                        13-SEP-1999 (first entry)
                                                                                                                                                                                                          Chlamydophila pneumoniae.
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Best Local Similarity
Matches 17; Conserv
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04-NOV-1998;
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                                                                                                                                                                                               Synthetic
                                           AAX96007;
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AAX96007/c
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The invention relates to an isolated polymucleotide molecule comprising a sequence encoding Lawsonia intracellularis HtrA, PonA, HypC, LysS, YcfW, Sequence encoding Lawsonia intracellularis HtrA, PonA, HypC, LysS, YcfW, ABC1 or Omp100 protein. The invention also relates to a genetic construct comprising a polymucleotide molecule that can be used to alter a Lawsonia or comprising a polymucleotide sequence of a htrA, ponA, hypC, lysS, OtfW, abc1 or omp100 gene, or its homologue, a substantial portion, or mutations capable of altering the above mentioned genes or a polymucleotide molecule comprising a sequence that naturally flanks in situ the ORF of the htrA, ponA, hypC, lysS, yoffW, abc1 or omp100 gene or its homologue. The invention also relates to a fusion protein of a colympetide of the invention further relates to a substantially pure polypeptide comprising an epitope of HtrA, PonA, HypC, LysS, YofW, ABC1 or Omp100 protein that is specifically reactive with anti-Lawsonia antibodies. The methods and compositions of the present invention are useful for the prevention and diagnosis of L. intracellularis infections in susceptible animals, such as pigs. Sequences ACA92344ACA92415.

C proteins of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a new isolated polynucleotide molecule which encodes Lawsonia intracellularis HtrA, PonA, HypC, LysS, YcfW, ABCl or Omp100 protein. The methods and compositions of the present invention are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated Lawsonia intracellularis polynucleotide and polypeptide, useful for the prevention and diagnosis of Lawsonia infections in susceptible animals, such as pigs.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60.0%; Score 13.2; DB 9; Length 21; 83.3%; Pred. No. 1.2e+04;
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05-NOV-1999; 99US-0163858P.
12-OCT-2000; 2000US-00689065.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention provides isolated polynucleotides encoding HtrA, PonA, HypC, LysS, YefW, ABC1 or Omp100 protein of Lawsonia intracellularis: The sequences can be used in vaccines for the prevention of Lawsonia intracellularis infection. The present sequence is an oligonucleotide described in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Primer, 88; antibacterial; HtrA; PonA; HypC; LysS; YcfW; ABC1; Omp100; Lawsonia intracellularis infection; Orf1; pig; PCR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                        Lawsonia intracellularis polynucleotide and encoded protein, used to
prevent Lawsonia intracellularis infection.
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Pred. No. 1.2e+04;
0; Mismatches 3; Indels
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05-NOV-1999; 99US-0163858P.
12-OCT-2000; 2000US-00689065.
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Best Local Similarity 83.3%;
Matches 15; Conservative (
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                    Lawsonia intracellularis.
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                                                                                                                                                                                                                                       (PPIZ ) PFIZER PROD INC.
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                                                               JP2001169787-A.
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ID AAF85459 standard; DNA; 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                             04-NOV-2004 (first entry)
                                                                                                                                                                                                                                                                   Lawsonia intracellularis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (PFIZ ) PFIZER PROD INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oryctolagus cuniculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2004-597336/58.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
es 15; Conserv
                                                                                                                                                                                                                                                                                                        JP2004229667-A.
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                                                                                                                                                                                                                                                                                                                                          19-AUG-2004
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                                                                                                                            ADR72987;
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                                                                        ADR72987
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This invention relates to a novel isolated polypeptide derived from Lawsonia intracellularis. The invention may be useful for the development of compounds with an antibacterial activity or a vaccine. Specifically claimed are L intracellularis proteins, such as HtrA, PonA, HypC, LysS, YcfW, ABC1 and Omp100 proteins. The invention may be useful for the development of vaccines, diagnostic agents, or in preventing L intracellularis infections in susceptible animals such as pigs, for example porcine proliferative enteropathy. The present sequence is that of a PCR primer which was used for amplification and/or sequencing of a region of L intracellularis DNA during the exemplification of the
useful for the prevention and diagnosis of L. intracellularis infections in susceptible animals, such as pigs. The present sequence is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                antibacterial; vaccine; HtrA; PonA; HypC; LysS; YcfW; ABC1; Omp100; diagnostic agent; infection; pig; porcine proliferative enteropathy; PCR; primer; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New Lawsonia intracellularis polypeptides, useful as vaccines, as diagnostic agents, or in preventing infections in susceptible animals such as pigs, e.g. porcine proliferative enteropathy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                      60.0%; Score 13.2; DB 10; Length 21; 83.3%; Pred. No. 1.2e+04; ive 0; Mismatches 3; Indels (
                                                                          Sequence 21 BP; 10 A; 3 C; 5 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 21 BP; 10 A; 3 C; 5 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                  Lawsonia intracellularis PCR primer SeqID50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 2; SEQ ID NO 50; 62pp; English
                                                                                                                                                                                4 TGTTACAGGTAGAAAGC 21
                                                                                                                                                                                                        TGGTACAGCAAGAAAGC 19
                                                                                                                                                                                                                                                                                                        ADJ66835 standard; DNA; 21 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-OCT-2000; 2000US-00689065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0160922P
                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                            Lawsonia intracellularis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INC.
PROD INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-895290/82.
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Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (PFIZ ) PFIZER
(PFIZ ) PFIZER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-OCT-1999;
05-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US6605696-B1
                                                                                                                                                                                                                                                                                                                                                                                 06-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rosey EL;
                                                                                                                                                                                                                                                                                                                                              ADJ66835;
                                                                                                                                                                                                                                                                       RESULT 6
ADJ66835
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The invention comprises the amino acid and coding sequences of the Lawsonia intracellularis proteins: HtrA, PonA, HypC, LysS, YcfW, ABC1, and Omp100. The DNA and protein sequences of the invention are useful for preventing Lawsonia intracellularis infection of animals (e.g. pig). The present DNA sequence was used in the exemplification of the invention. NOTE: The present sequence is not shown in the specification but was obtained from the Japanese Patent Office.
                                                                                                                                                                                                  HtrA; PonA; HypC; LysS; YcfW; ABC1; Omp100; infection; primer; probe; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nucleotide sequence that encodes HtrA, PonA, HypC, LysS, YcfW, ABC1 or Omp100 protein or its essential portion, useful as diagnostic agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Motilin receptor; gastrointestinal disease; gastric motility disorder; gastroparesis; irritable bowel syndrome; diarrhoea; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Polynucleotide in unique region in exon 1 of rabbit motilin receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel isolated polynucleotide comprising Lawsonia intracellularis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 21 BP; 10 A; 3 C; 5 G; 3 T; 0 U; 0 Other;
                                                                                                                                                 sequence #41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 2; SEQ ID NO 50; 55pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 TGGTACAGCAAGAAAGC 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BP.
ВР
                                                                                                                                                 Lawsonia intracellularis DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-OCT-1999; 99US-0160922P.
20-OCT-2000; 2000JP-00320736.
                                                                                                                                                                                                                                                                                                                                                                                                               26-MAR-2004; 2004JP-00092095.
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10-MAY-2001

21

4 TGTTACAGGTAGAAAAGC

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AAS99071;
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                                                                                                                                                                                                                          RESULT 10
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                                                                                                                                                                              AAF85456-60 represent polynucleotide sequences from the unique region of exon 1 of a rabbit motilin receptor gene. The specification describes an unique sequence present in exon 1 of the motilin receptor, which is not present in human or Sphaeroides nephelus 7557 motilin receptor sequences. The unique nucleic acid sequence is useful for measuring the ability of a compound to affect motilin receptor activity. Motilin receptor polynucleotides and polypeptides are used to identify therapeutic compounds which are useful for treating gastrointestinal diseases and disorders such as gastric motility disorders, gastroparesis, irritable bowel syndrome, and diarrhoea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human prostate cancer (HPC)2 nucleic acids, polypeptides, and antibodies, useful for treatment and diagnosis of prostate cancer.
                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                          Novel polypeptides related to dog and rabbit motilin receptor polypeptide, comprising unique regions from dog and motilin receptor amino acid sequence, useful for identifying compounds for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; mouse; prostate cancer predisposing gene; HPC2;
human chromosome 17p; gene therapy; peptide therapy; drug design;
PCR primer; sequencing primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human HPC2 cDNA exon 18 mutation screening primer SEQ ID NO: 157
                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                    Length 22;
                                                                                                                                                                                                                                                                                                                                       0: Indels
                                                                                                                                                                                                                                                                                                Sequence 22 BP; 2 A; 7 C; 5 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                   59.1%; Score 13; DB 4; Le 100.0%; Pred. No. 1.5e+04; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Teng DHF, Simard J, Rommens JM;
                                                                                                                                                               Claim 17; Page 22; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99WO-US026055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98US-0107468P
                              99US-0162264P.
          25-OCT-2000; 2000WO-US029426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MYRI-) MYRIAD GENETICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                 AAA60336 standard; DNA; 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                              Ouery Match
Best Local Similarity 100.
Watches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                           21
                                                                                                                                                                                                                                                                                                                                                                              CAGGTAGAAAAGC 1
                                                                                                                                                                                                                                                                                                                                                           9 CAGGTAGAAAAGC
                                                 (MERI ) MERCK & CO INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-376481/32.
                                                                                          WPI; 2001-343479/36.
                                                                                                                                           diarrhea in humans
                                                                      Mckee K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200027864-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tavtigian SV,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-NOV-1998;
                              29-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAA60336;
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The invention relates to a human prostate cancer predisposing gene coding for an HPC2 polypeptide. The DNA and protein sequences are useful as diagnostic reagents for identifying a mutant HPC2 nucleotide sequence in a suspected mutant HPC2 allele by comparing the sequence of the suspected mutant HPC2 allele with a wild-type HPC2 sequence. The sequences are also useful for detecting an alteration in HPC2, where the alteration is associated with cancer in a human. The method involves analysing an HPC2 gene or an HPC2 gene expression product from a tissue of the human. The HPC2 gene is useful as a marker for prostate cancer and can be used in gene therapy techniques to suppress neoplastic growth of recipient cells which carry the mutant HPC2 allele. The sequences represent primers used in the methods of the invention, cDNA encoding human and mouse HPC2 and cDNA encoding HPC2 paralogues and orthologues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                           The present sequence is a primer used in the isolation of the human and murine prostate cancer predisposing genes HPC2 and Mm.HPC2. The human version of the gene is found on chromosome 17p. Some alleles cause a predisposition to cancer, particularly prostate cancer. This gene and its protein can be used in peptide and gene therapy for cancer patients, as well as being useful as diagnostic tools (both for cancer sufferers and those with a predisposition to the disease) and in the production of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel nucleic acid sequence encoding HPC2 polypeptide, which is marker for prostate cancer, is useful in gene therapy techniques to restore HPC2 normal levels by which neoplastic growth is suppressed in recipient cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; mouse; HPC2; prostate cancer; neoplastic growth; cytostatic; se gene therapy; prostate cancer predisposing gene; chimpanzee; gorilla; sequencing primer; PCR primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ..
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 58.2%; Score 12.8; DB 3; Length 19; Best Local Similarity 87.5%; Pred. No. 1.9e+04; Matches 14; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 19 BP; 2 A; 6 C; 4 G; 7 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Simard J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 8, Page 74; 239pp; English.
Example 5; Page 61; 157pp; English.
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(HOSP-) HOSPITAL FOR SICK CHILDREN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-MAY-2001; 2001WO-US014602.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 ATGTTACAGGTAGAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-066599/09.
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                                                                                                                                                                                                                                                                                                                                                                      cancer drugs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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Matches

S

RESULT 11 AAT33010/c

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The present invention relates to a new method of making selectively randomised synthetic oligonucleotides. The method involves deprotecting starting material at 3' position, which is coupled to support in nucleic acid synthesiser, coupling dinuclectide phosphoramidite to 3' position, deprotecting the new 3' position of extended oligonucleotide, coupling mononucleotide phosphoramidite to the 3' position and repeating coupling steps until desired length oligonucleotide is obtained. The method of the invention is useful for making selectively randomised synthetic cligonucleotides. Unlike prior art techniques, the method provides randomised oligonucleotides without the problems of NNN randomisation, without having to resort to complicated resin-splitting procedures or the use of low coupling efficiency trinucleotide phosphoramidites. The present nucleic acid sequence represents one of a collection (ABK87646. ABK87669 and ABK87671-ABK87676) of synthetic oligonucleotides that were used in the invention for selective randomisation of zinc finger protein
                                                                                                                                                                                                                                                                                                                                                                                                                                             Making selectively randomized synthetic oligonucleotide by utilizing phosphoramidite dinucleotide and mononucleotide synthesis strategy, where a deprotecting step is performed after each coupling step.
Synthetic oligo #21, for selective randomisation of zinc finger protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transforming growth factor-beta 3 antisense oligonucleotide, SEQ ID 75.
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                                         Selectively randomised synthetic oligonucleotide; NNN randomisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58.2%; Score 12.8; DB 6; Length 20; 61.1%; Pred. No. 1.9e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seguence 20 BP; 1 A; 5 C; 2 G; 6 T; 0 U; 6 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 3; Fig 1B; 42pp; English.
                                                                   resin-splitting; zinc finger; ss
                                                                                                                                                                                                                                                                                                                       (SANG-) SANGAMO BIOSCIENCES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21
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                                                                                                                                                                                                                                                                                12-SEP-2000; 2000GB-00022330.
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TSYKCGAGKYAGAAAAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADA66516 standard; DNA; 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-507792/54.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
les 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                   Isalan M;
                                                                                                                                                      WO200222634-A1
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modified base
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                                                                                                                                                                                               21-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
                                                                                                               Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADA66516;
                                                                                                                                                                                                                                                                                                                                                               Choo Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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          셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The primers AAT33009-10 were used to amplify a fragment of the gene encoding a mouse SRY-related protein (AAT33007). This primer corresp. to bases 7156-7175 of the mouse gene. The amplified fragment was used to screen a mouse genomic library. The screen isolated 4 EcoRI fragments of 2.3, 2.8, 3.5 and 1.5 kb covering the gene. Sequence analysis revealed a 240 bp HMG box sequence between bases 7154-7393. Similarity with the thuman SRY HMG box sequence resulted in primers being generated to amplify the human SRY HMG box sequence for use as a probe to isolate the bowine SRY-related gene (AAT33008). The mouse and bowine genes are useful for determining the sex of an animal prior to birth
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mouse, SRY, primer, PCR, polymerase chain reaction, amplification, probe, HMG box; human, bovine, sex; animal, birth; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bovine and mouse Sry-related DNA - useful for detecting e.g. the sex of
                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                               58.2%; Score 12.8; DB 6; Length 19; 87.5%; Pred. No. 1.9e+04; ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58.2%; Score 12.8; DB 2; Length 20; 87.5%; Pred. No. 1.9e+04; ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 20 BP; 4 A; 6 C; 4 G; 6 T; 0 U; 0 Other;
        Sequence 19 BP; 2 A; 6 C; 4 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (KACH-) KACHIKU JUSEIRAN ISHOKU GIKUTSU KENKYUKU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 2; Page 6; 21pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                               Mouse SRY-related gene primer 2.
                                                                                                                                                                                                                                                                                  AAT33010 standard; DNA; 20 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22
                                                                                                                                     3 ATGTTACAGGTAGAAA 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94JP-00319525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94JP-00319525
                                                                                                                                                                   19 ATGTCACAGGCAGAAA 4
                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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                                                                                           14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                l Similarity 87.5
14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1996-336575/34.
                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      unborn animals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JP08154685-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-NOV-1994;
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                                                                                                                                                                                                                                                                                                                                                                     23-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                            AAT33010;
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Best Local S
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Matches

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Walker MG:

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The invention relates to a method of predicting clinical outcome for a patient diagnosed with cancer by determining the expression level of one cor more genes, or their expression products, selected from p53BP2, cathepsin B, cathepsin L, Ki6/7/MiBL, and thymidine Kinase in a cancer tissue obtained from the patient, normalized against control gene(s), and compared to the amount found in a reference cancer tissue set. The specification also discloses an array comprising polynucleotides by printing genes: FOXMI, PRAME, B612, STK15, CEGP1, Ki-CT, GSTMI, CA9, PR, BBC3, MBL1, SURV, GATA3, TFRC, YB-1, DPYD, GSTM3, CRESKEN, Sro, Chk1, IDI, BERRI, P27, CCMBI, XIAP, Chk2, CDC25B, IGFIR, CCC, MR93A, NRKB65B, BRCA2, EGFR, TK1, VDR, Contig51037, pENTI, EPHXI, IFIA, CCCH, HIPPI, IGFBP3, GTSB, HerZ and DIABLO, immobilized on a solid surface. The methods are useful for predicting clinical outcome for a satient diagnosed with cancer, classifying cancer, and predicting the clikelihood of long-term survival of a breast cancer patient, or a patient cancer patient, or a patient cancer patient.
                                                                                   Predicting clinical outcome for a patient diagnosed with cancer comprises determining the expression level of one or more genes, and compared to the amount found in a reference cancer tissue set.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PCR primer to amplify a human cancer prognostic marker DNA SeqID 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human; primer; PCR; prognostic marker; BGFR; epidermal growth factor receptor; cancer; gene expression profiling; microarray; head and neck cancer; colon cancer; metastatic spread;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        positive invasive breast cancer. This sequence corresponds to an oligonucleotide used in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58.2%; Score 12.8; DB 10;
87.5%; Pred. No. 1.9e+04;
rative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 21 BP; 5 A; 6 C; 5 G; 5 T; 0 U; 0 Other;
Shak S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Baselga J;
                                                                                                                                                                                  Disclosure; SEQ ID NO 230; 198pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GENO-) GENOMIC HEALTH INC.
(VALL-) VALL HEBRON UNIV HOSPITAL.
  Kiefer MC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shak S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADP27751 standard; DNA; 21 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-NOV-2002; 2002US-0427090P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 TACAGGTAGAAAAGCC 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-AUG-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTCTGGTAGAAAAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                neoplastic disease; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Baker JB, Cronin MT,
  Cronin MT,
                                             WPI; 2003-767536/72.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2004-420643/39
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO2004046386-A1.
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  Baker JB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADP27751;
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    g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to antisense oligonucleotides (ADA66459-ADA66609), which inhibit Transforming Growth Factor (TGF) beta-3 sepression. The oligonucleotides are useful for inhibiting the expression of TGF-beta3 in cells or tissues, and for treating an animal having a disease condition associated with TGF-beta3, e.g. a hyperproliferative disorder such as cancers of lung, liver, colon, oesophagus, pancreas, breast, skin or haematopoletic, atherosclerosis, rheumatoid arthritis, preeclampsia and fibrosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel antisense compound which is targeted to nucleic acid encoding transforming growth factor beta-3, and inhibits expression of TGF-beta 3, useful for treating a condition associated with TGF-beta 3, e.g. cancer.
                                               /notē= "This oligonucleotide has a phosphorothioate backbone and 2-"methyoxyethyl (2'-MOE) wings at the 5' and 3' ends, which are 5 nucleotides in length. Also all cytidine residues are 5-methylcytidines"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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58.2%; Score 12.8; DB 10; Length 20;

Best Local Similarity 87.5%; Pred. No. 1.9e+04;

Matches 14; Conservative 0; Mismatches 2; Indels (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 20 BP; 2 A; 5 C; 4 G; 9 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 3; Page 88; 154pp; English.
       /*tag= a
/mod_base= OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BP.
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18-SEP-2002; 2002US-0412049P.
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                                                                                                                                                                                                                                                          2002WO-US022423
                                                                                                                                                                                                                                                                                                    14-JUL-2001; 2001US-00906158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADG89282 standard; DNA; 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 TACAGGTAGAAAAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18 TACAGGAGAGAAATCC
                                                                                                                                                                                                                                                                                                                                                  (ISIS-) ISIS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                               Freier SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-229569/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO2003078662-A1
                                                                                                                                                                 WO2003008544-A2
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                                                                                                                                                                                                                                                          12-JUL-2002;
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                                                                                                                                                                                                            30-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                               Monia BP,
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RESULT 14 ADG89282/c

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Length 21; IndelB

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This invention relates to a novel method concerning prognostic markers associated with EGRR (epidermal growth factor receptor) positive cancer. Specifically, it refers to a gene expression profiling method that can provide a prediction as to whether a patient is likely to respond well to treatment with an EGRR inhibitor. The present invention describes the commandate of the RNA transcript of at least one gene selected from the group of CD4445, CD4446, DR5, GR01, KR17, LAMC2 or their products thereof. It further provides a cDNA microarray contraining mamed genes that represent prognostic transcripts which are useful for determining whether a patient diagnosed with an EGRR expressing head or neck cancer or colon cancer exhibits elevated or cancer expression levels of these genes compared to normal. As such, these methods are also useful for prognosing or predicting the likelihood of cancer-attributable death or prognosing or predicting the likelihood of cancer-attributable death or prognession, including recurrence and metastatic spread of a neoplastic disease, as well as drug resistance. This oligonucleotide sequence is a PCR primer used to amplify a human PCR amplicon DNA sequence used as a prognostic cancer marker, given in an exemplification of the invention.
Prognosing a patient with EGFR-expressing colon cancer comprises subjecting a sample comprising EGFR-expressing cancer cells to quantitative analysis of the expression level of the RNA transcript of at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 21 BP; 5 A; 6 C; 5 G; 5 T; 0 U; 0 Other;
                                                                                                                                                           Claim 54; SEQ ID NO 188; 113pp; English.
                                                                                          least one gene e.g., CD44v3.
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                                                       Gaps
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Query Match 58.2%; Score 12.8; DB 12; Length 21; Best Local Similarity 87.5%; Pred. No. 1.9e+04; Matches 14; Conservative 0; Mismatches 2; Indels (
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22
7 TACAGGTAGAAAAGCC
                TTCTGGTAGAAAAGCC
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ADR00153 standard; DNA; 21 BP
                                                                                                                                                                                                                                                                                                              (first entry)
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                                                                                                                                                                                                             ADR00153;
RESULT 16
                                                      ADR00153/N

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Breast cancer; human; 88; probe; COX2.

WO2004065583-A2

14-JAN-2004; 2004WO-US000985 05-AUG-2004.

15-JAN-2003; 2003US-0440861P. (GENO-) GENOMIC HEALTH INC

UYRU-) UNIV RUSH MEDICAL CENT.

Cronin MT; Baker JB, Shak S, Cobleigh MA,

WPI; 2004-593480/57.

Predicting likelihood of long-term survival of a breast cancer patient without the recurrence of breast cancer by determining the expression level of prognostic RNA transcripts or their expression products in a breast cancer tissue sample.

Claim 33; SEQ ID NO 191; 125pp; English

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The present invention relates to a method for predicting the likelihood of long-term survival of a breast cancer patient without the recurrence of breast cancer. The method comprises determining the expression level of one or more prognostic RNA transcripts or their expression products in a breast cancer tissue sample obtained from the patient. The prognostic RNA transcript is the transcript of one or more genes, e.g. TP513BP2, CR SRP, CD68, Bcl2, KRT14, RIZ1, ALB1, SURV, BBC3, IGFIR, p27, GATA3, CCGP1, STK15, GSTM1, FHT7, RIZ1, ALB1, SURV, BBC3, IGFIR, p27, GATA3, CCGP1, STK15, GSTM1, FHT7, RIZ1, ALB1, SURV, BBC3, IGFIR, p27, GATA3, CCGP1, STK, CD68, CCCGP1, STK, CD68, CCCCC, CKRT19, TS, Herz, KKK10, beta-catenin, gamma-catenin, Green or more of GRB7, CD68, CCCC, CKM19, FBXO5, or DR5, where expression of one or more of CTS1, CKM1, ALB1, CCNB1, MCM2, FBXO5, Herz, STK15, SURV, EGFR, MYBL2, CTS1, CKM1, ALB1, CCNB1, MCM2, FBXO5, Herz, STK15, SURV, EGFR, MYBL2, CCTS1, CKM1, BCM2, FBXO5, Herz, STK15, SURV, EGFR, MYBL2, CCTS1, CKM1, GATA3, CATA3, CA
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Internal Primer (SCAIP) sequencing method for direct sequence analysis of
large multi-exon genes from genomic DNA samples and identifying mutations
in multi-exon genes e.g. the dystrophin gene, CAPN3 gene and DYSF gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Characterizing a nucleic acid region, useful for detecting genetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    / Match 58.2%; Score 12.8; DB 13; Length 21; Local Similarity 87.5%; Pred. No. 1.9e+04; nes 14; Conservative 0; Mismatches 2; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; SCAIP; dystrophin; Duchenne Muscular Dystrophy; DMD; Becker Muscular Dystrophy; BMD; PCR; primer; ss; Single Condition Amplification/ Internal Primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Von Niederhausern A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 21 BP; 5 A; 6 C; 5 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 1; Page 34; 174pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dunn DM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DMD region PCR primer, SEQ ID 311.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-DEC-2003; 2003WO-US040278.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 TACAGGTAGAAAGCC 22
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invention
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       Dystrophy (DMD) and Becker Museular Dystrophy (BMD). Mutations in the CAPN3 gene, encoding calpain (calcium-activated neutral protease) result can limb-girdle muscular dystrophy type 2A (LGMD2A) and mutations in the DYSF gene, encoding dysferlin, result in limb-girdle muscular dystrophy type 2A (LGMD2A) and mutations in the DYSF gene, encoding dysferlin, result in limb-girdle muscular dystrophy type 2B (LGMD2B). The method comprises bringing into contact in each of the reaction chambers an amplicon from a different one of the amplicant or reactions and one or more internal sequencing primers corresponding to the amplicon and analysing the sequences of the amplicans. The method allows for the rapid, accurate, and economical canalysis of any large multi-exon gene. It is also useful in detecting genetic mutations in any large multi-exon gene. It is also useful for the identification and analysis of specific individual genomic mutations including deletions, point mutations, or its combinations, gene complexes with multiple exons/introms spanning large genomic regions. The present sequence is a PCR primer, used in the method of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               G protein coupled receptor; GPCR; signal transduction pathway; G protein; Alzheimer's disease; Parkinson's disease; diabetes; dwarfism; colour blindness; retinal pigmentosa; asthma; depression; schizophrenia; sleeplessness; hypertension; anxiety; stress; renal failure; cardiovascular disorder; neural disorder; oncology disorder; immune disorder; neuroprotective; gene therapy; PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This invention relates to novel G protein coupled receptors (GPCRs) and their encoding nucleotide sequences. Many medically significant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New nucleic acid, useful for manufacturing a medicament for preventing, treating or ameliorating a medical condition e.g., neural disorder.
                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human G-protein coupled receptor (GPCR) related PCR primer Seg ID44.
 Mutations in the dystrophin gene result in both Duchenne Muscular
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                                                                                                                                                                                                                                                                      57.3%; Score 12.6; DB 12; Length 20; 78.9%; Pred. No. 2.4e+04; ive 0; Mismatches 4; Indels C
                                                                                                                                                                                                                                             Sequence 20 BP; 3 A; 4 C; 6 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mintier GA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    ADD18145 standard; DNA; 20 BP
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26-NOV-2001; 2001US-0333417P.
06-DEC-2001; 2001US-0338367P.
                                                                                                                                                                                                                                                                                                                                                20 TCTTACAAGCAGAAAGGCC
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Matches 15; Conservative
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                                                                                                                                                                                                                                                                          Query Match
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biological processes are mediated by proteins participating in signal transduction pathways involving G proteins. GPCRs are one of the largest receptor superfamilies known. These receptors are biologically important and malfunction of these receptors results in diseases such as Alzheimer's, Parkinson's, diabetes, dwarfism, colour blindness, retinal pigmentosa and asthma. They are also involved in depression, schizophrenia, sleeplesaness, hypertension, anxiety, stress, renal failure and other cardiovascular, neural, oncology and immune disorders. A modulator of the GPCRs of the invention may have neuroprotective activity whilst the sequences of the invention may be useful for gene cherapy. The invention may also be useful for manufacturing a medicament for preventing, treating or ameliotating a medical condition. The present sequence is that of a PCR primer which was used for amplification of a certain of a gene encoding a human GPCR during the exemplification of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Pred. No. 3e+04;
0; Mismatches 1; Indels (
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Matches 13; Conservative
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RESULT 21
AAQ61732
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                                         The invention relates to an isolated human G protein-coupled receptor collypsecide and its encoding polyuncheoride, including the full length proteins rains the start methionine (and the region of the polybuncheoride encoding this protein region). The proteins are designated HGRBMY10-1, HGRBMY41-1, HGRBMY41-1, HGRBMY41-2, HGRBMY41-1, HGRBMY41-2, HGRBMY41-2, HGRBMY41-1, HGRBMY41-2, HGRBMY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene specific PCR primer for a nucleic acid encoding a novel GPCR of
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Pred. No. 3e+04;
0; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ethylene insensitivity related PCR primer SEQ ID No 32.
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                         Example 4; SEQ ID NO 92; 290pp; English.
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ABT16558 standard; DNA; 21 BP.
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Best Local Similarity
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ABT16558/c
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\mathbb{R}^{\frac{1}{2}}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel mutant or transformed plant comprising mutated forms of edf1, edf2, edf3 and edf4 genes, and having decreased ethylene sensitivity, such that its fruit ripens more slowly than wild-type version of the plant.
Mutant; transformed plant; ethylene-response DNA-binding factor; edf1; edf2; edf3; edf4; fruit; transgenic plant; floral industry; fruit processing industry; floral senescence; flower longevity; decreased floral initiation; post-harvest; transportation; PCR; primer;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seguence 21 BP; 6 A; 4 C; 4 G; 7 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 35; 85pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAQ61732 standard; cDNA; 18 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-MAY-2002; 2002WO-US014592.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-MAY-2001; 2001US-0289364P.
08-MAY-2001; 2001US-0289835P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GCATGTTACAGGTA 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Stepanova AN, Ecker JR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCATGTTACACGTA
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                                                                                                                                                                                                                                                                                                         WO200289555-A2.
                                                                                                                                                                                                                                  Unidentified
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                                                                                                                                                                                                                                                                                                                                                                                           14-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    invention
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Synthetic.
Hepatitis E virus.
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                                                                                                                                                                                                                                                                                                                                                                                                      02-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9846761-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-OCT-1998.
                                                                                                                                                                                                    -1780 and
                                                                                                                                                                                                                                                                                                                                                                                AAV71653;
            Isolated
                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                         RESULT 23
                                                                                                                                                                                                                                                                                                                                                    AAV71653
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                                                                                                                                                                                                                                                                                                                                                              8
                                                                                                                                                                                                          The sequences given in AAQ45198-200 and AAQ61687-777 are primers which were used in the isolation and amplification of the genomic sequence of the hepatitis E virus (HEV) strain SAR-55. These primers were based on sequences derived from the SAR-55 strain and a strain from Burma (BUR-121). The amplified sequence contains three open reading frames (GRFs). The proteins encoded by this sequence can be used to stimulate the production of protective antibodies upon injection into a mammal that would serve to protect the mammal upon challenge with wild type HEV. The proteins can be used for detection and diagnosis of HEV infection. This CDNA was isolated from primates innoculated with stool suspensions
                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                              Purified hepatitis B strain SAR-55 virus - used to develop prods. for use in detection, diagnosis, vaccines and therapy of hepatitis {\tt E} virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hepatitis E virus, HEV, SAR-55 strain, enteric transmission, structural region, antigen, detection, antibody, vaccine, immunisation, infection, primer, Burma-121, polymerase chain reaction, PCR, ss.
                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                     Query Match 55.5%; Score 12.2; DB 2; Length 18; Best Local Similarity 82.4%; Pred. No. 3.7e+04; Matches 14; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HEV strain Burma-121 derived reverse primer 133 (ORF-1).
                                                                                                                                                                                                                                                                                                                                                    Sequence 18 BP; 8 A; 5 C; 3 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (USSH ) US DEPT HEALTH & HUMAN SERVICES
                                                                                                      Emerson SU, Purcell RH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tsarev SA, Emerson SU, Purcell RH;
                                                                                                                                                                                         Example 1; Page 39; 114pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                 5 GTTACAGGTAGAAAGC 21
                                                                                                                                                                                                                                                                                                                                                                                                                                     Grracagecagaaacc 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAT27443 standard; DNA; 18 BP.
                                        93WO-US008849.
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                                                            92US-00947263
                                                                                 (USSH ) US SEC DEPT HEALTH
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                                                                                                                          WPI; 1994-118462/14.
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WO9406913-A2
                                         17-SEP-1993;
                                                             18-SEP-1992;
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                   31-MAR-1994.
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                                                                                                       TBarev SA,
                                                                                                                                                                    infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 22
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$X4X4X4X4X4X4X4X4X4X4X4X4X4X4X4X4X4X
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequences AAV71605 to AAV71698 represent primers used for PCR amplification of the hepatitis E virus (HEV) DNA SAR-55 encoding the reading frame (DRF) proteins ORF-1, ORF-2 and ORF-1. A host organism transformed or transfected with a recombinant expression vector containing the SAR-55 nucleic acid can be used to produce the HEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hepatitis E virus, HEV, SAR-55; diagnostic agent, vaccine, antibody, passive immunisation; open reading frame; ORF; PCR primer, ss.
and purified hepatitis E virus strain SAR-55 DNA - encodes c protein useful in diagnosis, prophylaxis and treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            55.5%; Score 12.2; DB 2; Length 18; 82.4%; Pred. No. 3.7e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HEV ORF proteins encoding DNA amplifying primer R 133 B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Emerson SU, Purcell RH, Tsarev SA, Robinson RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 18 BP; 8 A; 5 C; 3 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (USSH ) US DEPT HEALTH & HUMAN SERVICES.
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                                                                                                                                                        Example 1; Page 42; 121pp; English.
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                                     antigenic protein useful in
hepatitis E virus infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 GTTACAGGTAGAAAGC
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nes 14; Conservative
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N.B. The SEQ ID NOS 2852, 2313, 2374, 3035, 3157, are not actually given a sequence in the Sequence Listing from the
          used as diagnostic agents and as vaccines for use against HEV infection. The detection of antibodies specific for HEV can be used for the diagnosis of infection and diseases caused by HEV, and for monitoring the progression of such disease. Such methods are also useful for monitoring the efficacy of therapeutic agents during the course of treatment of HEV infection and disease in a mammal. The antibodies can be used for detection or for passive immunisation of mammals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel biallelic markers used to construct a high density disequilibrium
especially ORF-2 protein. The recombinant HEV proteins can be
                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human biallelic marker upstream amplification primer SEQ ID NO:4779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human genome; biallelic marker; high density disequilibrium map; genomic map; haplotype; phenotype; polymorphic base; genotyping; haplotyping; hybridisation; identification; characterisation; amplification; single nucleotide polymorphism; SNP; PCR primer;
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                                                                                                                                                                                                                 55.5%; Score 12.2; DB 2; Length 18; 82.4%; Pred. No. 3.7e+04; ive 0; Mismatches 3; Indels
                                                                                                                                                                          Sequence 18 BP; 8 A; 5 C; 3 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chumakov I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 8; Page 1250; 2745pp; English.
                                                                                                                                                                                                                                                                                                  5 GTTACAGGTAGAAAGC 21
                                                                                                                                                                                                                                                                                                                                       GTTACAGCCAGAAACC 18
                                                                                                                                                                                                                                                                                                                                                                                                                                         AAZ70423 standard; DNA; 18 BP
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                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     map of the human genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-013267/01
                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     diagnosis; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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23-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-SEP-2001
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                                                                                                                                                                                                                                                                                                                                               Human; Talin; antimicrobial; antiinflammatory; cytostatic; inhibitor; antisense gene therapy; infection; inflammation; Talin inhibitor; tumour; antisense oligonucleotide; phosphorothioate; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New antisense compound useful for inhibiting expression of Talin and for preventing or delaying infection, inflammation or tumor formation.
                                                                            Gaps
                                                                                                                                                                                                                                                                                                                   Human Talin antisense phosphorothioate oligonucleotide SEQ ID NO:44.
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/note= "2'-methoxyethyl (2'-MOE) nucleotides"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "2'-methoxyethyl (2'-MOE) nucleotides"
                                       55.5%; Score 12.2; DB 3; Length 18; 82.4%; Pred. No. 3.7e+04; ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mod_base= OTHER
/note= "phosphorothioate backbone"
           Seguence 18 BP; 6 A; 0 C; 9 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 15; Col 41; 46pp; English.
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                                                                                                                                         rereadaceracadade 17
                                                                                                                                                                                                                       BP
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                                                                                                           4 TGTTACAGGTAGAAAAG
                                                                                                                                                                                                                      ABN89231 standard; DNA; 20
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/*tag= b
                                                                                                                                                                                                                                                                                      (first entry)
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                                                           Local Similarity 82.4
les 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ISIS-) ISIS PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-470102/50.
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modified_base
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                                                                                                                                                                                                                                                                                      29-AUG-2002
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                                                                                                                                                                                                                                                       ABN89231;
                                              Query Match
                                                                                                                                                                                                          ABN89231/c
                                                                                                                                                                                                                                                                                                                                                                                                                     Homo
                                                                              Matches
                                                                                                                                                                                         RESULT 25
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ADC65754
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequences ADG90460-ADG90539 represent phosphorothioate targeted to the human talin gene, which inhibit its expression. The antisense were designed to target different regions of human talin RNA, and were analysed for their effect on talin expression by quantitative real-time PCR. Talin is a cytoplasmic protein which links cytoskeletal proteins extracellular matrix to other cells. It is thought to be involved in the regulation of cellular adhesion and cell morphology. Talin is highly
         oligonucleotide, having 2'-methoxyethyl (2'-MOE) wings of 5 nucleotides at the 5' and 3' ends and a 10 nucleotide deoxy gap in the middle, which is used in an example from the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "This oligonucleotide has a phosphorothioate backbone and 2-methyoxyethy1 (2-MOE) wings at the 5' and 3' ends, which are 5 nucleotides in length. Also all cytosine nucleotides are 5-methylcytosines"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            encoding human Talin, useful for inhibiting the expression of human Ta
and for treating a human having a disease or condition associated with
represents a human Talin antisense chimeric phosphorothioate
                                                                                                        Gaps
                                                                                                                                                                                                                                                                                      Human talin phosphorothioate antisense oligonucleotide, SEQ ID NO:44.
                                                                                                                                                                                                                                                                                                              Human; talin; cellular adhesion; muscle strength; cardiac function;
                                                                                                                                                                                                                                                                                                                                                            antisense therapy; phosphorothioate; antisense oligonucleotide; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antisense oligonucleotides targeted to nucleic acid molecules
                                                                                                        ö
                                                                                                                                                                                                                                                                                                                         cardiomyocyte; platelet; prostate; androgen downregulation; prostate cancer; talin-related disorder; capression inhibition; cellular adhesion-related disorder; expression inhibition;
                                                                               ch 55.5%; Score 12.2; DB 6; Length 20; 1 Similarity 82.4%; Pred. No. 3.8e+04; 14; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cowsert LM;
                                                          Seguence 20 BP; 3 A; 8 C; 4 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 15; SEQ ID NO 44; 114pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rothlein R, Kishimoto TK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (ISIS-) ISIS PHARM INC.
(BOEH ) BOEHRINGER INGELHEIM PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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                                                                                                                               4 TGTTACAGGTAGAAAG 20
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                                                                                                                                               TGTTGCAGGCAGCAAAG
                                                                                                                                                                                                     ADG90494/c
ID ADG90494 standard; DNA; 20
                                                                                                                                                                                                                                                               (first entry)
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                                                                                 Query Match
Best Local Similarity
Matches 14; Conserv
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modified_base
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                                                                                                                                                                                                                                         ADG90494;
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                                                                                                                                                                                           RESULT
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                           subcellular distribution differs between resting non-adhesive platelets and activated adhesive platelets. It could also play a major role in determining muscle strength and cardiac function as it has been found to participate in the transmission of contractile force to the extracellular matrix in cardiomyocytes, and exhibits mechanical loading-dependent expression at myotendinous junctions. The expression of talin is downregulated by androgens in prostate tissues, a phenomenon known to contribute to the development of prostate cancer. The oligonaclectides of the invention are useful for diagnosis, prevention and treatment of talin related disorders, such as those related to callular adhesion. The present sequence represents a human c-Ha-ras phosphorothicate antisense oligonuclectide used as a positive control in determining optimal oligonuclectide concentration for a particular cell line.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention comprises antisense oligonucleotides that are targeted to the nucleic acid encoding transforming.growth factor beta (TGF-beta) receptor II. The antisense oligonucleotides of the invention are useful for treating: hyperproliferative disorders (e.g. breast cancer), or an autoimmune disorder (e.g. rhematoid arthritis). The present DNA sequence represents a 2'-O-methoxyethyl gapmer oligonucleotide with a phosphorothioate backbone that is targeted to human TGF-beta receptor II.
expressed in platelets, and may play a role in platelet adhesion as its
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Transforming growth factor beta-receptor II, useful for preparing a
composition for treating hyperproliferative disorder e.g., lung, liver,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      transforming growth factor beta receptor II; TGF-beta receptor II; hyperproliferative disorder; breast cancer; autoimmune disorder; rheumatoid arthritis; 2'-0-methoxyethyl gapmer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human TGF-beta receptor II targeted antisense oligonucleotide #31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 20 BP; 3 A; 8 C; 4 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      55.5%; Score 12.2; DB 6; 82.4%; Pred. No. 3.8e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 3; SEQ ID NO 50; 141pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              human; antisense oligonucleotide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      phosphorothioate backbone; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 TGTTACAGGTAGAAAG 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGTTGCAGGCAGCAAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            colon or gastric cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wyatt JR;
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Best Local Similarity
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Human myosin X-derived oligonucleotide SEQ ID 1721.
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                                                                                                                                                                                                  WO200285308-A2.
                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                         31-OCT-2002
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                                                                                                                                                                                                                                                                                                                                                                                                      Nyce JW,
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ABD22709/c
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#X4X4X#
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to a method for detecting microorganisms using primers (ADF90918-ADF91145). The method is used for detecting microorganisms (bacteria, fungi, protozoa, viruses) which cause diarrhoea symptoms, and pathogenic microbe of food poisoning. The method can be used to detect unspecified microbes, or specific pathogens, or for the simultaneous detection of many kinds of microorganism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rapid, sensitive detection of specific or unspecified microbes causing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        diarrhea and food poisoning, using primers which target universal and specific genes, and amplifying by PCR under heat cycle conditions suitable for many detections.
                                                                               Gaps
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Pred. No. 3.8e+04;
0; Mismatches 3; Indels (
                                   55.5%; Score 12.2; DB 10; Length 20; 82.4%; Pred. No. 3.8e+04; ive 0; Mismatches 3; Indels (
Seguence 20 BP; 7 A; 4 C; 5 G; 4 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                   Microorganism detection PCR primer, SEQ ID 15.
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                                                                                                                                                                                                                                                              BP.
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ID ABZ86479 standard; DNA; 20 BP
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82.4%;
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                                                                               14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clostridium botulinum
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Best Local Similarity
Matches 14; Conserv
                                                          Best Local Similarity
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                                       Query Match
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ADP90933
ADP90933
AC ADP90933
AC ADP90

                                                                               Matches
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The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonucleotide antisense to the initiation codon, coding region, 5' or 3' end genomic flanking regions, 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an antiinflammatory steroid and ubiquinone. A composition of the invention has antiinflammatory, antiallergic, antiasthmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a comparing a respiratory, and cytostatic activity. The composition may have a conse in antisense gene therapy. The composition is useful for treating or preventing a respiratory, lung or therapeutic respiratory effect of an autiinflammatory steroid in a subject, for reducing levels of condition, also of, or reducing sensitivity to adenosine, reducing levels of denosine receptor, producing bronchodilation, increasing levels of ubiquinone or lung surfactant in a subject's tissue, or treating bronchoconstriction, lung allergies, or a respiratory disease or condition. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at figure.
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Human, antisense; lung dysfunction; nasal airway dysfunction; antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic; antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy; antisense gene therapy; respiratory; lung; adenosine sensitivity; adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pabalan J, Aguilar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       55.5%; Score 12.2; DB 10; Length 20; 82.4%; Pred. No. 3.8e+04; tive 0; Mismatches 3; Indels 0
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                                                                                                                                                                                                                                        lung inflammation; respiratory disease; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Katz E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 15; SEQ ID NO 1721; 872pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    i Y, Sandrasagra A, Ka
Tang L, Shahabuddin S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-APR-2002; 2002WO-US013135.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-APR-2001; 2001US-0286137P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (EPIG-) EPIGENESIS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 TGTTACAGGTAGAAAG
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This invention describes a novel composition (a) a first active agent, comprising oligonucleotides, effective for alleviating bronchoconstruction, respiratory tract inflammation, allergies and reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors, surfactant depletion or hyposecretion, when administered to a mammal. The oligonucleotides are derived from a gene encoding or regulating expression of a target polypeptide associated with lung airway or lung dysfunction or cancer and can be anti-sense to the corresponding mRNA. The invention also describes a kit, that comprises: (a) a delivery device, in separate containers, (b) the oligonucleotides, (c) instructions for adding a carrier and for use of the kit. The composition of the invention has antiallergic, antiinflammatory, antiasthmatic, analgesic, hypotensive, immunosuppressive and cytostatic activity, is a beta-adrenergic agonist. The composition is useful for preventing or treating a respiratory, lung or malignant disease. The administered or the composition of treating a respiratory, lung or malignant disease. composition comprises oligo and is administered to reduce the production or availability, or to increase the degradation of the target mRNA or to reduce the amount of target polypeptide present in the lungs. The pulmonary obstruction, and/or bronchoconstriction and/or lung inflammation, allergies and/or surfactant hypoproduction are associated with a disease or condition such as pulmonary vasoconstriction, inflammation, allergies, asthma, impeded respiration, respiratory distress syndrome, pain, oystic fibrosis, allergic rhinitis, pulmonary hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary the oligonuclectides into products that free adenosine into the system e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to prevent any unwanted effects due to it respiratory tract inflammation; adenosine sensitivity; lung; cancer; surfactant depletion; antiallergic; antinflammatory; antiasthmatic; analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis; beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction; respiratory distress syndrome; allergic rhinitis; pulmonary hypotremaion; emphysema; chronic obstructive pulmonary disease; cancer; bronchitis; pulmonary transplantation rejection; ss; primer. transplantation rejection, pulmonary infections, bronchitis or cancer. The reduced adenosine content of the anti-sense oligos corresponding to thymidines present in the target RNA serves to prevent the breakdown of Pharmaceutical composition for treating asthma, has antisense oligonuclectide containing less percentage of adenosine, targeted to nucleic acids associated with lung airway or lung dysfunction, and antisense; bronchoconstriction; allergy; hyposecretion; pain; Claim 15; SEQ ID NO 1721; 763pp; English. Li Y, Sandrasagra A, K. Tang L, Shahabuddin S; 23-APR-2002; 2002WO-US013143. 24-APR-2001; 2001US-0286036P. (EPIG-) EPIGENESIS PHARM INC bronchodilating agent WPI; 2003-093058/08 WO200285309-A2 Homo sapiens. 31-OCT-2002 Miller S, Nyce JW, Human:

ö Score 12.2; DB 11; Length 20; Pred. No. 3.8e+04; Indels Sequence 20 BP; 8 A; 4 C; 2 G; 6 T; 0 U; 0 Other; Mismatches ö 55.5%;

/mod_base= OTHER /note= "Phosphorothioate backbone where all cytidine Antisense; Talin; muscular disorder; haematologic disorder; cardiac disorder; hyperproliferative disorder; cancer; human; phosphorothioate; 88. /mod_base= OTHER 1/note= "2'-methoxyethyl (2'-MOE) nucleotides" 16. 20 /*tag= c /*tag= c $not\overline{e} = "2' - methoxyethyl (2' - MOE) nucleotides'$ Human Talin antisense oligonucleotide, ISIS #109143 residues are 5-methylcytidines" Location/Qualifiers /mod base= OTHER BP 30-OCT-2000; 2000US-00702251. 11-SEP-2003; 2003US-00415463 20 18 TTTTACATGTAGCAAAG ...5 *tag= a (first entry) Ω .699/c ADP85699 standard; DNA; *tag= BENNETT C F. COWSERT L M. US2004110705-A1 Key modified_base modified base modified_base sapiens 10-JUN-2004 26-AUG-2004 Synthetic ADP85699; (BENN/) (COMS/) Ношо RESULT 31 ADP85699,

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Katz E, Pabalan J, Aguilar

New compounds, particularly antisense oligonucleotides targeted to nucleic acid encoding talin, useful for treating muscular, cardiac, hematologic, or hyperproliferative disorders. nucleic acid hematologic,

Cowsert LM;

Bennett CF,

WPI; 2004-440384/41.

Example 15; SEQ ID NO 44; 48pp; English.

acid molecule encoding human Talin to and inhibit its expression. The invention is useful for treating a disease or condition associated with Talin such as a disease or condition e.g. muscular, haematologic, cardiac or hyperproliferative disorder such as cancer. The present sequence is an antisense oilgonucleotide targeted to human Talin DNA. invention relates to novel antisense compounds targeted to a nucleic

Score 12.2; DB 12; Pred. No. 3.8e+04; 0; Mismatches 3; Sequence 20 BP; 3 A; 8 C; 4 G; 5 T; 0 U; 0 Other; ö 55.5**%**; 82.4**%**; Local Similarity Query Match Best Loca Matches

14; Conservative

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Gaps

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Length 20; Indela

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Gaps

8

20

4 TGTTACAGGTAGAAAG | ||||| |||| ||||

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The invention relates to a set of novel map-related biallelic markers, preferably located on obesity disorder-associated chromosomal regions on estimates, i. I o and 19. The markers are useful for genotyping or estimating the frequency of an allele in a population, for detecting an association between a genotype or haplotype and a phenotype, e.g. a disease involving drug responses, obesity or disorders related to obesity, such as hyperuricaemia, digestive pathology, hepatic function disorders, cancer, cardiovascular disease, hypertension, hyperlipidaemia, insulin disorders, atheromatous disease and cardiac insufficiency. The marker are useful for detecting a statistical correlation between a biallelic marker haplotype and a phenotype and/or between a biallelic marker haplotype and a phenotype. This sequence represents a PCR primer used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Set of novel map-related biallelic markers, preferably located on obesity disorder-associated chromosomal regions on chromosomes 3, 10 and 19, useful, for e.g. detecting statistical correlations between marker allele and a phenotype.
drug response; hyperuricaemia; digestive pathology; hypertension; cancer; hepatic function disorder; cardiovascular disease; hyperlipidaemia; PCR; insulin disorder; atheromatous disease; cardiac insufficiency; primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cold-inducible promoter activity; promoter; non-translational region; Saccharomyces cerevisiae; yeast; vector; expression system; RNA production regulation; molecular mechanism; low-temperature inducibility; PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chumakov I, Abderrahim H, Bihain B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 12.2; DB 6; Length 21;
Pred. No. 3.8e+04;
0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amplify a human obesity-associated biallelic marker
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Query Match
Best Local Similarity
"Active Tay, Conservative Tay, Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Blumenfeld M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-155043/20.
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                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                               24-JAN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cohen D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention is concerned with a number of human single nucleotide polymorphisms (SNPs) which the inventors identified in human genes. These SNPs can be used in disease diagnosis and prediction of an individual's susceptibility to disease, in forensic and paternity testing and in genetic mapping. In particular, the SNPs of the invention can be used to diagnose susceptibility to diseases of the cardiovascular, endocrine and neurological systems, such as coronary artery disease, echizophrenia, cancer, autoimmune diseases, Alzheimer's and Parkinson's
                                                                                                                                                                                                                                                                                                                                                                                                                Single nucleotide polymorphism; SNP; human; genetic disease;
disease susceptibility; cardiovascular system; endocrine system;
neurological system; forensic testing; paternity testing; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acid selected from one of 106 genes comprising single nucleotide polymorphisms, allele-specific oligonucleotides to the genes are useful for phenotypic correlations, forensics, paternity testing, medicine and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; obesity associated-biallelic marker; chromosome 10; obesity; 88;
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Patil N, Sklar P;
                                                                                                                                                                                                                                                                                                                                                     Single nucleotide polymorphism PCR primer #1921
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                                                                                                                                              AAC73052 standard; DNA; 21 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens,
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Matches
                                                                            RESULT 32
                                                                                                           AAC73052

IID AAC7

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AAC7

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AAZ65654 to AAZ69578 represent human biallelic markers from the present invention, which contain a polymorphic base at position 24 of their nucleotide sequences. AAZ69579 to AAZ740 represent amplification conclined as a parameter. The biallelic markers of the invention have a variety of uses: they can be used for high density mapping of the human genome, and in complex association studies and haplotyping studies which are useful in determining the genetic basis for disease states. Compositions and mathods of the invention can also be useful for the accomplex asponses to an also be useful for the dentification of the targets for the development of pharmaceutical agents and disapnostic methods, as well as the characterisation of the cificacious responses to and side effects from pharmaceutical agents acting on a disease as well as other treatment. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and 3367, are not actually given a sequence in the Sequence Listing from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic oligo #15, for selective randomisation of zinc finger protein.
                                                                                                                                                                                                                                                                                    Novel biallelic markers used to construct a high density disequilibrium map of the human genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Selectively randomised synthetic oligonucleotide; NNN randomisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   54.5%; Score 12; DB 3; Length 20; 75.0%; Pred. No. 4.7e+04; tive 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 20 BP; 6 A; 6 C; 1 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                            Chumakov I;
                                                                                                                                                                                                                                                                                                                                                                    Claim 8; Page 2297; 2745pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               resin-splitting; zinc finger; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GCATGTTACAGGTAGAAAG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTATGTCTGAGGTATAAAG 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (SANG-) SANGAMO BIOSCIENCES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABK87660 standard; DNA; 20 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-SEP-2000; 2000GB-00022330.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-SEP-2001; 2001WO-GB004084.
                                                                   98US-0082614P.
98US-0109732P.
                    99WO-IB000822.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24-SEP-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 75.0
Matches 15; Conservative
                                                                                                                                                                                            Blumenfeld M,
                                                                                                                                                                                                                                           WPI; 2000-013267/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-507792/54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isalan M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200222634-A1.
                                                                                                                                           (GEST ) GENSET
                    21-APR-1999;
                                                                   21-APR-1998;
                                                                                             23-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-MAR-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABK87660;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20
                                                                                                                                                                                            Cohen D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Choo Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 36
ABK87660/c
요
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ઠે
                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes a DNA fragment with a cold-inducible promoter activity which occurs in the non-translational region in the 5'-
bystream side of a gene selected from the 259 specified Saccharomyces cerevisiae genes given in the specification (G) e.g. YALO14C and YPRZ00C.

Also described: (1) a similar DNA fragment containing: (a) a DNA derived from any of the specified DNA fragments (G) but with some bases deleted, substituted or added; or (b) a DNA hybridisable with a DNA fragment containing a base sequence complementary to any of the specified DNA fragment containing a cis sequence of DNA sequence of B: GAGATGAG; (3) a DNA fragment containing a cis sequence of bus sequence of B: GAGATGAG; (3) a DNA fragment with cold-inducible promoter activity containing; (a) a DNA fragment in (2) but with some bases deleted, an expression vector containing any of the DNA fragment in (2); (4) an expression vector containing any of the DNA fragment in (2); (4) an expression vector containing any of the DNA fragment in (2); (4) an expression vector containing any of the postession vector; (5) production by culturing the transformant at a low temperature; and (7) controlling RNA production by culturing the transformant at a low temperature; and for temperature inducible in constructing vectors and expression systems to produce difficult-to-obtain proteins and for regulating RNA production as well as in studying the molecular mechanism of low-temperature inducibility. The present sequence represents a PCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                  Yeast-originated promoters with cold-inducible activity for constructing vectors and expression systems to produce difficult-to-obtain proteins and for regulating RNA production.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human biallelic marker downstream amplification primer SEQ ID NO:9693.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human genome; biallelic marker; high density disequilibrium map; genomic map; haplotype; phenotype; polymorphic base; genotyping; haplotyping; hybridisation; identification; characterisation; amplification; single nucleotide polymorphism; SNP; PCR primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             primer which is used in an example from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          55.5%; Score 12.2; DB 12; Length 22; 82.4%; Pred. No. 3.8e+04; ive 0; Mismatches 3; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 22 BP; 8 A; 3 C; 7 G; 4 T; 0 U; 0 Other;
                                                                                                                      (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
                                                                                                                                                                        Kawasaki K;
                                                                                                                                                                                                                                                                                                                                                                          Example 2; SEQ ID NO 1; 106pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20
                                                                                                                                                                     Ohgiya S, Goda T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAZ75337 standard; DNA; 20 BP
                       13-MAY-2003; 2003WO-JP005956
                                                                        28-JUN-2002; 2002JP-00191383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 TGTTACAGGTAGAAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14; Conservative
                                                                                                                                                                                                                      WPI; 2004-083056/08.
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Matches 14; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 diagnosis; se
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9954500-A2
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                                                                                                                                                                     Sahara T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAZ75337;
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RESULT 35 AAZ75337,

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01-JUL-2003; 2003WO-US020865. 01-JUL-2002; 2002US-0392813P.

(PHAA) PHARMACIA CORP

Kane CD;

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The present invention relates to a new method of making selectively randomised synthetic oligonucleotides. The method involves deprotecting starting material at 3 position, which is coupled to support in nucleic card synthesiser, coupling dinucleotide phosphoramidite to 3 position and repeating coupling monouncleotide phosphoramidite to the 3 position and repeating coupling monouncleotide phosphoramidite to the 3 position and repeating coupling reps until desired length oligonucleotide is obtained. The method of the invention is useful for making selectively randomised synthetic oligonucleotides. Unlike prior art techniques, the method provides candomised oligonucleotides without the problems of NNN randomisation, without having to resort to complicated resin-splitting procedures or the use of low coupling efficiency trinucleotide phosphoramidites. The present nucleic acid sequence represents one of a collection (ABK87646-ABK87669 and ABK87676) of synthetic oligonucleotides that were used in the invention for selective randomisation of zinc finger protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
Making selectively randomized synthetic oligonucleotide by utilizing phosphoramidite dinucleotide and mononucleotide synthesis strategy, where a deprotecting step is performed after each coupling step.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                human; ss; liver related homologue-1; LRH1; NR5A2; antisense; phosphorothioate; 2' MOE; breast cancer; dyslipidaemia; atherosclerosis; low HDL; high density lipoprotein; high LDL; hypercholesterolaemia; gall stone; triglyceridaemia; obesity; hepatitis; hepatocellular carcinoma; aromatase; cytostatic; antilipaemic; antiarteriosclerotic; anorectic; hepatotropic; litholytic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mod_base= OTHER /note= "OTHER= 2' methoxyethyl (2' MOE) nucleotides. All cytidine nucleobases are 5-methylcytidine."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "OTHER= 2' methoxyethyl (2' MOE) nucleotides. All
cytidine nucleobases are 5-methylcytidine."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antisense DNA oligo used to modulate human LRH1 expression SeqID 2166.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                             54.5%; Score 12; DB 6; Length 20; 66.7%; Pred. No. 4.7e+04; ive 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'mod_base= OTHER
'label= OTHER= phosphorothioate backbone
                                                                                                                                                                                                                                                                                                                                                                                                                           Seguence 20 BP; 1 A; 6 C; 3 G; 6 T; 0 U; 4 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= c
/mod_base= OTHER
                                                                               Example 3; Fig 1B; 42pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 TGTTACAGGTAGAAAGC 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N
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ADJ17616 standard; DNA; 20 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antiinflammatory; virucidal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 66.7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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This invention relates to novel antisense compounds useful for modulating the expression of liver related homologue-1 (LRH1) and splice variants thereof. Specifically, it refers to compositions 8-30 nucleobases in clength that target a portion of an active site on the nucleic acid molecule encoding LRH1 (also known as NRBA2). LRH1 is a monomeric orphan complex receptor protein that functions as a tissue specific corphan actor. The present invention describes antisense coligonucleotides that comprise at least one modified internucleoside oligonucleotides that comprise at least one modified sugar moiety, a 2'-0-methoxyethyl (2' MOE) and at least one modified sugar moiety, confines the sancisense compounds are useful for treating or diagnosing a disease associated with LRH1, such as breast cancer, disploidaemia, atherosclerosis, low HDL (high density lipoprotein), high corporation, hyperrolesterolaemia, gall stones, confining an expectation as well as hepatocellular carcinoma or a condition associated with aromatase activity, Accordingly, these compositions exhibit cytostatic, antilipaemic, antiarteriosclerotic, anorectic, hepatotropic, clibolytic, antilipaemic, antiarteriosclerotic, anorectic, hepatotropic, coligonucleotides sequence is an antisense DNA oligo used to modulate the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           vascular endothelial growth factor; ss; antisense compound; phosphorothioate linkage; 2'-O-methoxyethyl sugar moiety; 5'-methylcytosine; antisense oligonucleotide; diabetes; immunological disorder; cardiovascular disorder; neurological disorder; tardiovascular disorder; neurological tisorder; ischaemia; reperfusion injury; cancer; angiogenic disorder; haemangioma; tumour angiogenesis; rheumatoid arthritis; atherosclerosis; psoriasis; fibrosis; myocardial infarction; wound healing; bone fracture; cartilage damage; tissue regeneration; organ regeneration; periodontal disease; gut regeneration; atrial fibrillation.
                                                                                                                                                                                                                                         New antisense oligonucleotides targeted to a nucleic acid encoding liver related homologue-1 (LRH1), useful for treating breast cancer, dyslipidemia, atherosclerosis, hypercholesterolemia, or hepatitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human VEGF co-regulated chemokine-1 DNA antisense oligonucleotide #620.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   54.5%; Score 12; DB 12; Length 20; 75.0%; Pred. No. 4.7e+04; tive 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               expression of the human LRH1 protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 20 BP; 4 A; 5 C; 4 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; VEGF co-regulated chemokine-1; VCC-1;
                                                                                                                                                                                                                                                                                                                                        Example 15; SEQ ID NO 2166; 909pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 ATGTTACAGGTAGAAAAGCC 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 75.0°
Matches 15, Conservative
                                                                                                                                                                                                     WPI; 2004-083058/08.
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matrix metalloproteinase; growth factor; reductase; scarring; cytostatic; antipsoriatic; dermatological; antiseborrheic; antidiabetic; virucide; antisickling; ophthalmological; keratolytic; gene therapy; viral wart; atopic dermatitis; actinic keratosis; squamous cell carcinoma; basal cell carcinoma; seborrheic wart; vitreoretinopathy; scar; sickle cell retinopathy; ss.
cell-cycle dependent kinase; cyclin; MMP;
                                                                                                                                                                                                                                                                                                                                                               26-OCT-2000; 2000WO-US029500.
                                                                                                                                                                                                                                                                                                                                                                                                               99US-0161532P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Robbins JM, Tritz R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               (IMMU-) IMMUSOL INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-300427/31.
                                                                                                                                                                                                                                                                     WO200130362-A2.
                                                                                                                                                                                                                                                                                                                                                                                                               26-OCT-1999;
                                                                                                                                                                                                 sapiens
                                                                                                                                                                                                                                                                                                                  03-MAY-2001
                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADO16516;
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                                                                                                                                                                                                 Ношо
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AD016516
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to an antisense compound targeted to a nucleic acid molecule encoding human vascular endothelial growth factor (VEGF) corregulated chemokine-1 (VCC-1), and which specifically hybridises with and inhibits the expression of VCC-1. The invention also relates to a composition comprising the antisense compound, a method of inhibiting the expression of VCC-1 in cells or tissues compound, a method of inhibiting the carries of VCC-1 in cells or tissues compound and a method of treating a human of varing a disease or condition associated with VCC-1 comprising a disease or condition associated with VCC-1 comprising comprises at least one modified of internucleoside linkage, preferably a phosphorothicate linkage. It also comprises at least one modified sugar moiety, preferably a 2'-0-comprises at least one modified sugar moiety, preferably a 2'-0-comprises at least one modified sugar moiety, preferably a 2'-0-comprises at least one modified sugar moiety, preferably a 2'-0-comprises at least one condition associated with VCC-1 such as diabetes, a chimeric oligonucleotide. The antisense oligonucleotide preferably contracting a disease or condition associated with VCC-1, such as diabetes, an immunological disorder, a cardiovascular disorder, a neurological disorder, a cardiovascular disorder, a neurological configurable of the sorder, inchemial or fibrosis after myocardial infarction. VCC-1 antisense oligonucleotides may also be used for wound healing, for treating periodomial diseases, for gut protection or regeneration, for treatment of Indig or liver fibrosis or for management of atrial fibrillation. This sequence represents an antisense management of atrial fibrillation. This sequence represents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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recognition site; target; ribozyme binding site; eye disease; vulnerary;
proliferative disease; skin disease; psoriasis; diabetic retinopathy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             igonucleotide targeted to DNA encoding the human VCC-1 polypeptide of
                                                                                                                                                                                                                                                                                                                                         New antisense compounds targeted to a nucleic acid molecule encoding vascular endothelial growth factor co-regulated chemokine-1 (VCC-1), useful for treating VCC-1-associated disorders, e.g. diabetes or a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 54.5%; Score 12; DB 12; Length 20; Best Local Similarity 75.0%; Pred. No. 4.7e+04; Matches 15; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VEGF hammerhead ribozyme recognition site SEQ ID NO:4514.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 20 BP; 6 A; 4 C; 3 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 4; SEQ ID NO 620; 336pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 ATGTTACAGGTAGAAAAGCC 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arciircaggiaarraagcc 20
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                                                                                                 19-AUG-2003; 2003WO-US025891.
                                                                                                                                                    19-AUG-2002; 2002US-0404484P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-SEP-2001 (first entry)
                                                                                                                                                                                                 (PHAA ) PHARMACIA CORP
                                                                                                                                                                                                                                                                                              WPI; 2004-192065/18.
                                                                                                                                                                                                                                                                                                                                                                                                                    neurologic disorder
       WO2004016224-A2.
                                                                                                                                                                                                                                                   Weinstein EJ;
                                                       26-FEB-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 39
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The present invention describes a method for treating a proliferative skin or eye disease and scarring. The method involves administering a ribozyme (1) which clasaves RNA encoding a cytokine involved in inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle dependent kinase, growth factor or a reductase, or administering a nucleic acid molecule (II) comprising a promoter operably linked to a nucleic acid segment encoding (I). (I) can have antipsoriatic, dermatological, cytostatic, antiseborrheic, antidiabetic, antisickling, dermatological, cytostatic, antiseborrheic, antidiabetic, antisickling, cophthalmological, vulnerary, keratolytic and virucide activities, and cleaves RNA encoding cytokine involved in inflammation. (I) can be used in gene therapy. (I) and (II) are useful for treating proliferative skin diseases such as psoriasis, atopic dermatitis, actinic keracosis, caquamous or basal cell carcinoma and viral or seborrheic wart. They can also be used for treating proliferative eye diseases such as diabetic retinopathy, virreoretinopathy, sickle cell retinopathy, correctinopathy, sickle cell retinopathy, of prematurity and retinal detachment, and for treating and preventing scarring such as keloid, adhesion and hypertrophic or hypertrophic burn and correcting and preventing scarring such as keloid, adhesion and hypertrophic or hypertrophic burn and correcting and preventing scarring such as keloid, adhesion and hypertrophic or hypertrophic burn and correcting and preventing and control or sequences used in the
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Treating proliferative skin or eye diseases and scarring, using ribozymes that cleave RNA encoding cytokines involved in inflammation, matrix metalloproteinases, growth factors and cell-cycle dependent kinases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; 4 synthesis-period; neuroblastoma; stage 4S; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match 54.5%; Score 12; DB 5; Length 21; Best Local Similarity 75.0%; Pred. No. 4.8e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 21 BP; 3 A; 9 C; 3 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
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                                                                                                                                                                                                                                    Example 1; Page 26; 408pp; English.
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                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to human nucleic acid sequences (1; ADO15739-ADO15912) obtained from 4 synthesis-period (stage 4S) of neuroblastoma cell. (I) is useful for prognosing and determining the progress stage of 4 synthesis-period of neuroblastoma. The present sequence is a primer, used to illustrate the invention.
                                                                                                                                                                                                                                                                          Novel nucleic acid obtained from 4 synthesis-period of neuroblastoma cells useful for prognosing and determining progress stage of neuroblastomas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 54.5%; Score 12; DB 12; Length 22; Best Local Similarity 100.0%; Pred. No. 4.8e+04; Matches 12; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 22 BP; 10 A; 6 C; 4 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                         Claim 8; SEQ ID NO 778; 455pp; Japanese.
                                                                                                                                                                 (HISM ) HISAMITSU PHARM CO LTD. (CHIB-) CHIBA PREFECTURE.
                                                                                                       30-OCT-2003; 2003WO-JP013932.
                                                                                                                                      30-OCT-2002; 2002JP-00316586.
                                                                                                                                                                                                                Nakagawara A, Ohira M;
                                                                                                                                                                                                                                                 WPI; 2004-390323/36.
                                          WO2004039975-A1.
                                                                        13-MAY-2004.
            Synthetic.
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Search completed: August 12, 2005, 08:58:58 Job time : 245 sec8

7 TACAGGTAGAAA 18 |||||||||||| 1 TACAGGTAGAAA 12

8 8

Sequence 19 Sequence 70 Sequence 70 Sequence 70 Sequence 70 Sequence 70 Sequence 27 Sequence 27 Sequence 27	Sequence 58 Sequence 69 Sequence 69 Sequence 69 Sequence 13 Sequence 21 Sequence 22 Sequence 22 Sequence 22 Sequence 26	Sequence Seq	Sequence 55 Sequence 11 Sequence 12 Sequence 12 Sequence 12 Sequence 12 Sequence 13 Sequence 13 Sequence 13 Sequence 14 Sequence 15 Sequence 16 Sequence 16 Sequence 16 Sequence 16 Sequence 16 Sequence 17 Sequence 18 Sequence 19 Sequen
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11111111111111111111111111111111111111	2 11.4 4 5 51.1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	25.55.55.55.55.55.55.55.55.55.55.55.55.5	74 11 50.0 75 11 50.0 76 11 50.0 77 11 50.0 80 11 50.0 80 11 50.0 81 11 50.0 82 11 50.0 83 11 50.0 84 11 50.0 84 11 50.0 8 8 10.8 49.1 8 9 10.6 48.2 9 6 10.6 48.2
GenCore version 5.1.6 ht (c) 1993 - 2005 Compugen Ltd. ch, using sw model , 2005, 08:29:02; Search time 95 Seconds (without alignments) 378.927 Million cell updates/sec	Gatgttacaggtagaaagcc 22 Gratgttacaggtagaaaagcc 22 ENTITY NUC pop 10.0 , Gapext 1.0 02784 segs, 818138359 residues ts satisfying chosen parameters: 487750 gth: 0 gth: 0 gth: 22	the No.* the State of the result being produced to the score of the result being produced by the score of the score distribution.	20 4 US-09-198-452A-5333 Sequence 5333, Ap 21 4 US-09-689-065B-50 Sequence 50, Appl 18 3 US-08-864-06157, Appl 18 3 US-08-864-0116-53 Sequence 53, Appl 18 3 US-08-809-223-53 Sequence 53, Appl 18 4 US-08-402-776-53 Sequence 53, Appl 18 4 US-09-422-978-4779 Sequence 53, Appl 18 4 US-09-422-978-4779 Sequence 53, Appl 18 4 US-09-316-765-53 Sequence 53, Appl 18 5 PCT-US93-08849A-53 Sequence 53, Appl 18 6 US-09-724-475-53 Sequence 53, Appl 20 3 US-09-724-475-53 Sequence 53, Appl 20 3 US-09-724-475-53 Sequence 53, Appl 20 3 US-09-722-978-673 Sequence 23, Appl 20 4 US-09-606-791-4514 Sequence 4514, Appl 20 3 US-09-422-978-6072 Sequence 6072, Appl 20 3 US-09-422-978-6072 Sequence 603, Appl 20 3 US-09-487-445-98 Sequence 702, Appl 20 3 US-09-487-445-98 Sequence 702, Appl 21 4 US-09-622-978-4514 Sequence 702, Appl 22 US-09-865-162-702 Sequence 703, Appl 23 US-09-865-162-702 Sequence 703, Appl 24 US-09-621-162-702 Sequence 703, Appl 25 US-08-985-162-702 Sequence 703, Appl 26 US-08-985-162-705 Sequence 703, Appl 27 US-08-985-162-705 Sequence 703, Appl 28 US-08-985-162-705 Sequence 703, Appl 29 US-08-985-162-705 Sequence 703, Appl 20 US-08-985-162-705 Sequence 703, Appl 20 US-08-985-162-705 Sequence 703, Appl 21 US-08-985-162-705 Sequence 703, Appl 21 US-08-985-162-705 Sequence 703, Appl 21 US-08-985-162-705 Sequence 703, Appl 29 US-08-985-162-705 Sequence 703, Appl 20 US-08-985-162-705 Sequence 703, Appl 20 US-08-985-162-705 Sequence 703, Appl 21 US-08-985-162-705 Sequence 703, Appl 22 US-08-985-162-705 Sequence 703, Appl 23 US-08-985-162-705 Sequence 703, Appl 24 US-08-985-162-705 Sequence 703, Appl 25 US-08-985-162-705 Sequence 703, Appl 26 US-08-985-162-705 Sequence 703, Appl 27 US-08-985-162-705 Sequence 703, Appl 28 US-08-985-162-705 Sequence 703, Appl 29 US-08-985-162-705 Sequence 703, Appl 20 US-08-985-162-705 S
Copyright OM nucleic - nucleic search Run on: August 12,	US 222 222 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Database : Issued Pater Listing firr 2: /cgn2_6/, 3: /cgn2_6/, 4: /cgn2_6/, 5: /cgn2_6/, 5: /cgn2_6/, 6: /cgn2_6/, 6: /cgn2_6/, 8: /cgn2_6/, Result Result No. Score Match Length No. Score Match Length	C 1 15.2 69.1 C 3 113.2 60.0 4 112.2 55.5 6 112.2 55.5 7 112.2 55.5 10 112.2 55.5 11 12.2 55.5 11 12.2 55.5 11 12.2 55.5 11 12.2 55.5 12 12.2 55.5 13 12.2 55.5 14 12.2 55.5 15 12.2 55.5 16 12.2 55.5 17 12.2 55.5 18 11.8 53.6 C 17 11.8 53.6 C 21 11.6 52.7 23 11.4 51.8 24 51.8 25 11.4 51.8

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APPLICANT: Rommens, Johanna M.

APPLICANT: Myriad Genetics, Inc.

TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
FILE REFERENCE: 2318-258
CURRENT APPLICATION NUMBER: US/09/564,805
CURRENT FILING DATE: 2000-05-05
PRIOR PAPLICATION NUMBER: 09/434,382
PRIOR PLING DATE: 1998-11-06
PRIOR APPLICATION NUMBER: 09/434,382
NUMBER OF SEQ ID NOS: 240
SOFTWARE: Patentin Ver. 2.0
SSED ID NO 157
TEDMAN: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 53, Application US/08840316

Sequence 53, Application US/08840316

Patent No. 6054567

GENERAL INFORMATION:
APPLICANT: Emerson. Suzanne U., Purcell, Robert H.,
APPLICANT: Taszev, Sergel. A., and Robinson, Robin A.
TITLE OF INVENTION: Recombinant Proteins Of
TITLE OF INVENTION: A Pakistani Strain Of Hepatitis E And Their
TITLE OF INVENTION: Use In Diagnostic Methods And Vaccines
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
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CURRENT APPLICATION NUMBER: US/08/840,316
FILING DATE: 11-APP-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: R.C.A.C.W. BOTK
REGISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 2026
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: FLOPPY DISK COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS'M-SOPTWARE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58.2%;
87.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 ATGTTACAGGTAGAAA 18
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INFORMATION FOR SEQ ID NO: S
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 87.5
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY
                                                                                                                                                                                                                                                                                                                                                                                                                                               CRGANISM: Homo sapiens US-09-564-805-157
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                                                                                                                                                                                                 Sequence 5333, Application US/09198452A

Patent No. 6559294

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments

TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, preverittle OF INVENTION: and treatment of infection

FILE REFERENCE: 9710-003-999

CURRENT APPLICATION NUMBER: US/09/198,452A

CURRENT FILING DATE: 1998-11-24

NUMBER OF SEQ ID NOS: 6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 50, Application US/09689065B

Facent No. 6605696

GENERAL INFORMATION: LAWSONIA INTRACELLULARIS PROTEINS AND RELATED METHODS AND TITLE OF INVENTION: LAWSONIA INTRACELLULARIS PROTEINS AND RELATED METHODS AND TITLE OF INVENTION: MATERIALS

TITLE OF INVENTION: MATERIALS

TITLE OF INVENTION: MATERIALS

CURRENT PRILING DATE: 2000-10-12

FRIOR PEPLICATION NUMBER: US Prov. 60/160,922

FRIOR APPLICATION NUMBER: US Prov. 60/163,858

FRIOR FILING DATE: 1999-11-05

NUMBER OF SEQ ID NOS: 112

SOFTWARE: Patentin version 3.2

SEQ ID NO 50

LENGTH: 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 69.1%; Score 15.2; DB 4; Length 20; Best Local Similarity 85.0%; Pred. No. 3.2e+02; Matches 17; Conservative 0; Mismatches 3; Indels
                                                                                     ALIGNMENTS
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Patent No. 6333403
PATENT INFORMATION:
APPLICANT: Tavtigian, Sean V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: DNA
; ORGANISM: Lawsonia intracellularis
US-09-689-0658-50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GCATGTTACAGGTAGAAAAG 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: DNA; Chlamydia pneumoniae; ORGANISM: Chlamydia pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tavtigian, Sean V.
Teng, David H.F.
Simard, Jacques
                                                                                                                                                                                         US-09-198-452A-5333/c
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US-09-564-805-157/C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 2
US-09-689-065B-50
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APPLICANT:
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TITLE OF INVENTION: Recombinant TITLE OF INVENTION: A Pakistani STITLE OF INVENTION: Use In Diagno NUMBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSEE: MORGAN & FINNEGAN STREET: 345 PARK AVENUE STREET: NEW YORK STATE: NEW YORK COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7
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INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY I
                                   APPLICANT: Tsarev,
APPLICANT: Suzanne
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GENERAL INFORMATION:
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| Patent No. 6207416
| GENERAL INFORMATION: A PAPLICANT: Tearer, Suranne U., Purcell, Robert H. APPLICANT: Suranne U., Purcell, Robert H. TITLE OF INVENTION: Recombinant Proteins Of TITLE OF INVENTION: A PARKstani Strain Of Hepatitis E And Their TITLE OF INVENTION: Wee In Diagnostic Methods And Vaccines NUMBER OF SEQUENCES: 107
| CORRESPONDENCE ADDRESS: ADDRESSEE: MORGAN & FINNEGAN, L.L.P. STREET: 345 PARK AVENUE
| CITY: NEW YORK | STATE: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                            ch 55.5%; Score 12.2; DB 3; Length 18; 1 Similarity 82.4%; Pred. No. 9.3e+03; 14; Conservative 0; Mismatches 3; Indels
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Pred. No. 9.3e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READBLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/809,523
FILING DATE: 03-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/1102
FILING DATE: 03-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/94
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/947,263
FILING DATE: 18-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Richard W. BOTK
REFERENCE/DOCKET NUMBER: 2026-4032US4
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 Dase pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTTACAGCCAGAAACC 18
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Local Similarity 82.4%;
nes 14; Conservative (
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STRANDEDNESS: single
                                       Query Match
Best Local Similarity
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Matches
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Sequence 53, Application US/08471971 Patent No. 6287759

US-08-471-971-53

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APPLICANT: Targer, Sergie, A., Emecon.,
APPLICANT: Suzanne U., Purcell, Robert H.
APPLICANT: Suzanne U., Purcell, Robert H.
TITLE OF INVESTION: Recombinant Processed of the specifies E And Their TITLE OF INVESTION: Recombinant Processed of the specifies E And Their TITLE OF INVESTION: Recombinant Processed of the specifies E And Their TITLE OF INVESTION: Recombinant Processed of the specifies E And Their TITLE OF INVESTION: Recombinant Processed of the specifies E And Their TITLE OF INVESTION: A PARLICANT OF THE STANDARD STREET: 345 PARK AVENUE
COMPITIES IN THE WORKEN E TINNEGAN STREET: BRANCH FORCESSED OF THE STREET APPLICATION OF TH
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Sequence 53, Application US/08470246

Patent No. 6696242

GENERAL INFORMATION

APPLICANT: Tarrev, Sergei. A., Emerson,
APPLICANT: Suzanne U., Purcell, Robert H.
TITLE OF INVENTION: Recombinant Proteins Of
TITLE OF INVENTION: Use In Diagnostic Methods And Vaccines
TITLE OF SEQUENCES: 107

NUMBER OF SEQUENCES: 107

CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 53, Application US/08316765
Patent No. Großers
GENERAL INFORMATION:
APPLICANT: Tsarev, Sergei. A., Emerson,
APPLICANT: Suzanne U., Purcell, Robert H.
TITLE OF INVENTION: A Pakistani Strain Of Hepatitis E And Their
TITLE OF INVENTION: Use In Diagnostic Methods And Vaccines
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55.5%; Score 12.2; DB 4; Length 18; 82.4%; Pred. No. 9.3e+03; tive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTY: USA

ZIP: 10154

COUNTY: USA

COUNTRY: USA

COMPUTER REDABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OFFRATIOR SYSTEM: PC-DOS/MS-DOS
SOFFWARE: WORDPERFECT 5.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,246
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US08/316,765
FILING DATE: 03-OCT-1994
CLASSIFICATION DATA:
APPLICATION NUMBER: US07/947,263
FILING DATE: 18-SEP-1992
CLASSIFICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION WHERE: 18-SEP-1992
CLASSIFICATION WHERE: 2056-4032US3
TELEPHONE: AND STATES A SERIES A 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MORGAN & FINNEGAN
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INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
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US-08-316-765-53
                                                               JS-08-470-246-53
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APPLICANT: Cohen, Daniel
APPLICANT: Blumenfeld, Marta
APPLICANT: Blumenfeld, Marta
APPLICANT: Blumenfeld, Marta
APPLICANT: Chumakov, Ilya
APPLICANT: Chumakov, Ilya
APPLICANT: Chumakov, Ilya
CURENT: Chumakov, Ilya
TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
CURENT APPLICATION NUMBER: US/09/422, 978
CURENT FILING DATE: 1999-10-20
EARLIER APPLICATION NUMBER: US 60/109,732
EARLIER PILING DATE: 1998-11-23
EARLIER PILING DATE: 1998-11-23
EARLIER PILING DATE: 1998-11-23
EARLIER PILING DATE: 1998-04-21
NUMBER OF SEQ ID NOS: 11796
SEQ ID NO 4779
LENGTH: 18
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; OTHER INFORMATION: upstream amplification primer 99-17762 for SEQ 845,
US-09-422-978-4779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 55.5%; Score 12.2; DB 3; Length 18; Best Local Similarity 82.4%; Pred. No. 9.3e+03; Matches 14; Conservative 0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                               CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/840,316
APPLICATION NUMBER: 08/840,316
FILING DATE: 11-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Richard W. Bork
REGISTRATION NUMBER: 36,459
REFERRNCE/DOCKET NUMBER: 2026-4255
TELECOMMUNICATION: INFORMATION:
                            MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/402,776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4779, Application US/09422978
Patent No. 6537751
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (212) 758-4800
TELEPAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 53: SEQUENCE CHARACTERISTICS: LENGTH: 18 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 82.4
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: primer_bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-422-978-4779
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US-09-402-776-53
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                                                                                                                                                                                                                                                                                                                                               55.5%; Score 12.2; DB 4; Length 18; 82.4%; Pred. No. 9.3e+03; tive 0; Mismatches 3; Indels
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                FILING DATE: 18-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Richard W. Bork
REGISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 2026-4032US4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 754-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 12.2; DB 5;
Pred. No. 9.3e+03;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 10154

ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIELE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/08849A
FILING DATE: 17-SEP-1993
FRIOR APPLICATION NUMBER: PCT/US93/08849A
FILING DATE: 18-SEP-1992
ATTORNEY/AGENT INFORMATION:
HAME: William S. Febler
REGISTRATION NUMBER: 26,728
REFERENCE/DOCKET NUMBER: 2026-4032 PCT
TELECHONE: (212) 751-6849
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 Dases pairs
                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQ ID NO: 53:
APPLICATION NUMBER: 07/947,263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 53, Application PC/TUS9308849A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 GTTACAGGTAGAAAGC 21
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Best Local Similarity 82.4%;
Matches 14; Conservative
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CITY: NEW YORK
STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 82.4
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: BIR
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APPLICANT: Tsarev, Sergei. A., Emerson,
Suzanne U., Purcell, Robert H.
TITLE OF INVENTION: Recombinant Proteins Of
A Pakistani Strain Of Hepatitis B And Their
USE IN Diagnostic Methods And Vaccines
NUMBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESS:
A PARK AVENUE
CITY: NEW YORK
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPPERATING SYSTEM: PC-DS/MS-DOS
SOPTWARB: WORDPEREET 5.1
CURRENT APPLICATION DATA:
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PRING DATE: 28 No. 6787145-2000
PRIOR APPLICATION DATA:
PILING DATE: «URKLOWN-
PAPLICATION NUMBER: 08/809,523
PILING DATE: «URKLOWN-
APPLICATION NUMBER: US08/316,765
PILING DATE: 03-0CT-1994
                                                                                                       COMPUTER READBLE FORM:
MEDIUM TYPE: FLOPPY DISK
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA: 08/316,765
PILING DATE: 03-OCT-1994
CLASSIFICATION NUMBER: US/08/316,765
PILING DATE: 03-OCT-1994
CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/316,765
FILING DATE: 18-SEP-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Richard W. BORK
REGISTRATION WUMBER: 36,459
REFERENCE/DOCKET NUMBER: 36,459
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 53, Application US/09724475
Patent No. 6787145
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S GTTACAGGTAGAAAGC 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Griacagccagaaaacc 18
      : 345 PARK AVENUE
NEW YORK
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EDNESS: single
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
                                              NEW YORK
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                                                                                              10154
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US-09-724-475-53
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                              CITY: NE
STATE: NI
COUNTRY:
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; OTHER INFORMATION: Antisense Oligonucleotide US-09-702-251-44
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TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                    19 TGTTGCAGGCAGGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: sing
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: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
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                                          FEATURE:
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                                                                                                                       FGT-US93-08849-53
; Sequence 53, Application PC/TUS9308849
; GENERAL INFORMATION:
    APPLICANT: Suzanne U., Purcell, Robert H.
    TITLE OF INVENTION: Recombinant Proteins Of
    TITLE OF INVENTION: A Pakistani Strain Of Hepatitis E And Their
    TITLE OF INVENTION: Use In Diagnostic Methods And Vaccines
    NUMBER OF SEQUENCES: 98
; CORRESPONDENCE ADDRESS:
    ADDRESSEE: MORGAN & FINNEGAN
    STREET: 345 PARK AVENUE
    CITY: NEW YORK

    STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Sequence 46, Application US/09702251
Sequence 46, Application US/09702251
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Lex M. Cowsert
TITLE OF INVENTION: ANTISENSE MODULATION OF TALIN EXPRESSION
FILE REPRENCE: RTS-0199:
CURRENT APPLICATION NUMBER: US/09/702,251
CURRENT FILING DATE: 2000-10-30
NUMBER OF SEQ ID NOS: 89
SEQ ID NO 44
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 55.5%; Score 12.2; DB 5; Length 18; Best Local Similarity 82.4%; Pred. No. 9.3e+03; Matches 14; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: BOCK, Richard, W.
REGISTRATION NUMBER: 2026-4032
REFERENCE/POCKET NUMBER: 2026-4032
TELEPONNINICATION INFORMATION:
TELEPONDIS: (212) 758-4800
TELEFAX: (212) 758-4800
TELEFAX: (212) 758-6849
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION UMBER: PCT/US93/08849
FILING DATE: 17-SEP-1993
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/947,263
FILING DATE: 18-SEP-1992
                               2 GTTACAGCCAGAAAACC 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 GTTACAGGTAGAAAGC 21
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  5 GTTACAGGTAGAAAGC 21
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US-09-702-251-44/c
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PCT-US93-08849-53
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     Length 20;
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                                                     Indels
                                                                                                                                                                       Sequence 23, Application US/08765340
; Sequence 23, Application US/08765340
; Patent No. 6150092
; GENERAL INFORMATION:
; APPLICANT: UCHIDA, K.,
; APPLICANT: UCHIDA, T.,
; APPLICANT: MARKA, Y.,
; APPLICANT: MARGUIDA, Y.,
; TITLE OF INVENTION: AN ANTISENSE NUCLEIC ACID
; TITLE OF INVENTION: COMPOUND
NUMBER OF SEQUENCES: 185
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
Query Match 55.5%; Score 12.2; DB 3; Best Local Similarity 82.4%; Pred. No. 9.5e+03; Matches 14; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: BATCHILI RELEASE #1.0, Version
SOFTWARE: PATCHILI RELEASE #1.0, Version
FILING DATE: 23-DEC-1996
PRIOR APPLICATION NUMBER: JP 145146/94
FILING DATE: 27-JUN-1994
PRIOR APPLICATION NUMBER: JP 311130/94
FILING DATE: 21-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: SERUNTAN, LESLIE
REGISTRATION NUMBER: 35,353
REGISTRATION NUMBER: 35,353
REFERENCE/DOCKET NUMBER: 1452-4005
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "synthetic DNA"
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APPLICANT: Cohen, Daniel
APPLICANT: Cohen, Daniel
APPLICANT: Blumenfeld, Marta
APPLICANT: Chumakov, Ilya
APPLICANT: Chumakov, Ilya
APPLICANT: Chumakov, Ilya
TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
FILE REFERENCE: GENSET.020CP1
CURRENT APPLICATION NUMBER: US/09/422, 978
CURRENT FILING DATE: 1999-10-20
EARLIER APPLICATION NUMBER: US 60/109,732
EARLIER APPLICATION NUMBER: US 60/109,732
EARLIER PILING DATE: 1998-11-23
EARLIER FILING DATE: 1998-11-23
EARLIER FILING DATE: 1998-04-21
NUMBER OF SEQ ID NOS: 11796
SEQ ID NO 6072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: primer_bind
LOCATION: 1..19
) OTHER INFORMATION: upstream amplification primer 99-8748 for SEQ 2138,
US-09-422-978-6072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 86.7%; Pred. No. 1.5e+04;
Matches 13; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 27, Application US/08477270
; Sequence 27, Application US/08477270
; Patent No. 5629158
; GENERAL INFORMATION:
    APPLICANT: UHLEN, Mathias
; TITLE OF INVENTION: COLID PHASE DIAGNOSIS OF MEDICAL;
TITLE OF INVENTION: CONDITIONS
; UNMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Roley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 16787/153 DFBC TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: Virginia
COUNTRY: USA
ZIP: 22313-029
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/261,010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
APPLICATION NUMBER: US 07/781,157
FILING DATE: 07-NOV-1991
ATTORNEY/AGENT INFORMATION:
             Sequence 6072, Application US/09422978
Patent No. 6537751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 GTTACAGGTAGAAA 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-477-270-27/c
JS-09-422-978-6072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 19
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; OTHER INFORMATION: downstream amplification primer 99-669 for SEQ 1828, in complemen
US-09-422-978-9693
                                                                                                                                                                            GENERAL INCORMATION:
APPLICANT: Cohen, Daniel
APPLICANT: Chen, Daniel
APPLICANT: Chumenfeld, Marta
APPLICANT: Chumenfeld, Marta
APPLICANT: Chumenfeld, Marta
APPLICANT: Chumenfeld, Marta
APPLICANT: Blumenfeld, Marta
FILER OF INVENTION: Biallelic markers for use in constructing a high density...
FILER PRERENCE: GENSET. 0200CPI
CURRENT FILING DATE: 1999-10-20
EARLIER APPLICATION NUMBER: US 60/109, 732
EARLIER FILING DATE: 1998-04-21
EARLIER FILING DATE: 1998-04-21
MUMBER: OF SEQ ID NOS: 11796
SEQ ID NOS: 11796
EARLIER FILING DATE: 1098-04-21
EARLIER FILING DATE: 1098-04-21
EARLIER FILING DATE: 1098-04-21
EARLIER FILING DATE: 1098-04-21
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APPLICANT: Tritz, Richard
APPLICANT: Tritz, Richard
TITLE OF INVENTION: RIBOZYME THERAPY FOR THE TREATMENT OF PROLIFERATIVE
TITLE OF INVENTION: SKIN AND EXE DISEASES
FILE REFERENCE: 480124.407
CURRENT APPLICATION NUMBER: US/09/696,791
CURRENT FILING DATE: 2000-10-25
NUMBER OF SEQ ID NOS: 4523
SEG ID NO 4514
LENGTH: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
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Set 12; DB 4; Length 21;
Best Local Similarity 75.0%; Pred. No. 1.2e+04;
Matches 15; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    54.5%; Score 12; DB 4; Length 20; ilarity 75.0%; Pred. No. 1.2e+04; Conservative 0; Mismatches 5; Indels
                                                                                                                              Sequence 9693, Application US/09422978 Patent No. 6537751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-696-791-4514/c
; Sequence 4514, Application US/09696791
; Patent No. 6770633
; GENERAL INPORMATION:
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     GCATGGTGGAGGTAGAGCAG 20
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ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: primer_bind
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Best Local Similarity
                                                                                     RESULT 16
US-09-422-978-9693/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
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RESULT 22
US-09-422-978-4544

i Sequence 4544, Application US/09422978

i Sequence 4544, Application US/09422978

i GENERAL INFORMATION:

APPLICANT: Cohen, Daniel

APPLICANT: Chumakov, Ilya

i TITLE OF INVENTION: Biallelic markers for use in constructing a high density...

FILE REFERENCE: GENSET.020CP1

CURRENT APPLICATION NUMBER: US/09/422,978

CURRENT FILING DATE: 1999-04-21

EARLIER APPLICATION NUMBER: US 60/109,732

EARLIER PILING DATE: 1999-04-21

EARLIER PILING DATE: 1999-04-21

EARLIER FILING DATE: 1999-04-21

EARLIER FILING DATE: 1998-04-21

NUMBER OF SEQ ID NOS: 11796

SERVIER APPLICATION NUMBER: US 60/082,614

EARLIER FILING DATE: 1998-04-21

IENGTH: 19
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                                                                  Gaps
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; OTHER INFORMATION: upstream amplification primer 99-15744 for SEQ 610,
US-09-422-978-4544
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              Score 11.6; DB 3; Length 19;
Pred. No. 1.9e+04;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Akhtar, Saghir
APPLICANT: Rell, Patricia
APPLICANT: Reswigen, James
TITLE OF INVENTION: ENYMATIC NUCLEIC ACID TREATMENT
TITLE OF INVENTION: OF DISEASES OR CONDITIONS RELATED
TITLE OF INVENTION: TO LEVELS OF PEIDERMAL GROWTH
TITLE OF INVENTION: TO LEVELS OF PEIDERMAL GROWTH
TITLE OF SEQUENCES: 1877
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52.7%; Score 11.6; DB 4; ilarity 77.8%; Pred. No. 1.9e+04; Conservative 0; Mismatches 4;
                                                               0; Mismatches
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MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Grorage
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 23
US-08-985-162-702
; Sequence 702, Application US/08985162
Patent No. 6057156
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
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                 Query Match 52.7%;
Best Local Similarity 77.8%;
Matches 14; Conservative
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CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 14; Conserv
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APPLICANT: Stich, Roger W.
APPLICANT: Stich, Roger W.
APPLICANT: Stich, Roger W.
APPLICANT: Rikihisa, Yasuko
TITLE OF INVENTION: Methods for Detecting Ehrlichia Canis and Ehrlichia Chaffeensis:
TITLE OF INVENTION: Vertebrate and Invertebrate Hosts
FILE REFERENCE: 22727/04069
CURRENT APPLICATION NUMBER: US/09/648,520E
CURRENT FILING DATE: 2000-08-25
NUMBER OF SEQ ID NOS: 51
SOFTWARE: PatentIn version 3.1
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Sequence 98 Application US/09487445

Patent No. 6258600

GENERAL INFORMATION:
APPLICANT: Hong Zhang
APPLICANT: Lex M. Cowsert

TITLE OF INVENTION: ANTISENSE MODULATION OF CASPASE 8 EXPRESSION
FILE REFERENCE: RTS-0107

CURRENT APPLICATION VUMBER: US/09/487,445

CURRENT FILING DATE: 2000-01-19

NUMBER OF SEQ ID NOS: 176

LENGTH: 20

LENGTH: 20
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86.7%; Pred. No. 1.5e+04;
tive 0; Mismatches 2; Indels
                 TELEX: 899149
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS.
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid;
DESCRIPTION: Synthetic DNA oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Antisense Oligonucleotide US-09-487-445-98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
; OTHER INFORMATION: synthetic sequence
US-09-648-520E-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 21
US-09-648-520E-29/c
; Sequence 29, Application US/09648520E
; Patent No. 6432649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity 86.73
Matches 13; Conservative
(703)683 - 4109
                                                                                                                                                                                                                                                                                                                               Query Match 53.6
Best Local Similarity 86.7
Matches 13; Conservative
                                                                                                                                                                                                                            ; IMMEDIATE SOURCE:
; CLONE: RIT 34
US-08-477-270-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 20
US-09-487-445-98
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 51.8%; Score 11.4; DB 3; Length 17; Best Local Similarity 61.5%; Pred. No. 2.3e+04; Matches 8; Conservative 4; Mismatches 1; Indels
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; Patent No. 6057156
; Patent No. 6057156
; GENERAL INFORMATION:
APPLICANT: Akhtar: Saghir
APPLICANT: Patenticia
APPLICANT: McSwiggen, James
TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT
TITLE OF INVENTION: TO LEVELS OF EPIDERMAL GROWTH
TITLE OF INVENTION: FACTOR RECEPTORS
TITLE OF INVENTION: FACTOR RECEPTORS
TITLE OF INVENTION: FACTOR RECEPTORS
TOWNBER OF SEQUENCES: 1877
CORRESPONDENCE ADDRESS:
ADDRESSE: Lyon & Lyon
Comment of the com
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COUNTY: LOS Angeles
COUNTY: U.S.A.
ZIP: 90071-2066
ZIP: 90071-2066
ZOMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 18.5" DISKette, 1.44 Mb
MEDIUM TYPERTY TYPERTY TYPERTY TYPERTY
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STREET: 633 West Fifth Street
STREET: Suite 4700
                                      TELEPHONE: (213) 489-1600
TELERAX: (213) 955-0440
TELEX: 67-3510
INFORMATION POR SEQ ID NO: 703:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GCATGTTACAGGT 13
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4 GCAUUUUACAGGU 16
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Best Local Similarity 61.5
Matches 8; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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EDNESS: single
GY: linear
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                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                              ;
TOPOLOGY:
US-08-985-162-703
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,162
FILING DATE: 04 December 1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION UNMBER: 60/036,476
FILING DATE: 31 January 1997
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 33,327
REFERENCE/DOCKET NUMBER: 330/107
REJECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELERAX: 67-3510
INFORMATION FOR SEQ ID NO: 702:
SEQUIENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 230/107
FELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 24
18-08-985-162-703
; Sequence 703, Application US/08985162
; Patent No. 6057156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 61.5:
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5 GCAUUTUACAGGU 17
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US-08-985-162-702
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APPLICANT: Pavco, Pam
APPLICANT: Standbomb, Jam
APPLICANT: Standbomb, Dan
APPLICANT: Standbomb, Dan
APPLICANT: Standbomb, Dan
APPLICANT: Standbomb, Dan
APPLICANT: Standbomb, Jaime
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
FILE REFERENCE: MBHB00,876-J (237/198)
CURRENT APPLICATION NUMBER: US/09/371,772B
CURRENT FILING DATE: 1995-10-26
PRIOR APPLICATION NUMBER: US 60/005,974
PRIOR FILING DATE: 1995-10-06
PRIOR FILING DATE: 1996-01-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51.8%; Score 11.4; DB 3; Length 17; 69.2%; Pred. No. 2.3e+04; tive 3; Mismatches 1; Indels
                 TREATMENT OF DISEASES OR CONDITIONS RELATED TO LEVELS OF VASCULAR ENDOTHELIAL GROWTH FACTOR 8502
     METHOD AND REAGENT FOR THE
                                                                                                                                                                                                                         COUNTRY: CALLLILLS

ZIP: 90071-206

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/584,040
FILING DATE: January 11, 1996
CLASSIFICATION S14
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/005,974
FILING DATE: October 26, 1995
ATTORNEY AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 218/064
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 79, Application US/09371772B
Patent No. 6566127
GENERL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
TITLE OF INVENTION: METHOD AND REJ
TITLE OF INVENTION: COMPITIONS REI
TITLE OF INVENTION: COMPITIONS REI
TITLE OF INVENTION: GROWTH FACTOR
NUMBER OF SEQUENCES: 8502
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 1534:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 TGTTACAGGTAGA 16
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5 UGAUACAGGUAGA 17
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Best Local Similarity 69.2
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                             Los Angeles
California
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US-09-371-772B-79
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                                                                                                             FILING DATE: 04 DECEMBER 1997

CLASSIFICATION: 514

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/036,476
FILING DATE: 31 January 1997
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 230/107
TELEPHONE: (213) 489-1600
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEFAX: (213) 855-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 705:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1534, Application US/08584040
Patent No. 6346398
GENERAL INFORMATION:
APPLICANT: Pavco, Pamela
APPLICANT: McSwiggen, James
APPLICANT: Stinchcomb, Dan T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 61.5-
Then 8; Conservative
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GCAUUUUACAGGU 14
         13
                             3 GCAUUUUACAGGU 15
         GCATGTTACAGGT
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US-08-584-040-1534
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Sequence 703, Application US/09401063

GENERAL INFORMATION:

APPLICANT: Rell, Patricia APPLICANT: Rell, Patricia APPLICANT: McSwiggen, James TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT TITLE OF INVENTION: TO LEVELS OF EPIDERMAL GROWTH TITLE OF INVENTION: TO LEVELS OF EPIDERMAL GROWTH TITLE OF INVENTION: FACTOR RECEPTORS

NUMBER OF SEQUENCES: 1877

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon STREET: G31/E00-18

CITY: Los Angeles

STREET: G31/E00-18

COUNTRY: U.S.A.

ZIP: 90071-2066

CONTRY: U.S.A.

MEDIUM TYPE: Storage

CONTRY TYPE: Storage

MEDIUM TYPE: Storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/985,162
FILING DATE: 04 December 1997
APPLICATION NUMBER: 60/036,476
FILING DATE: 31 January 1997
ATTORNEY/AGENT INPORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REGISTRATION NUMBER: 32,327
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELER: 67-3510
INPORMATION FOR SEQ ID NO: 702:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOPTWARE: FESTENG for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/401,063
                                                                     COMPUTER: IBM COMPALIBLE
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FRAELSEQ for Windows 2.0
CURRENT APPLICATION DATA:
FILING DATE:
CLASSIFICATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/985,162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 51.8%;
Best Local Similarity 61.5%;
Matches 8; Conservative
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s gcauuuuacaggu 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 17 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-401-063-702
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APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Rabozyme Pharmaceuticals, Inc.
APPLICANT: Pavco, Pam
APPLICANT: Bacobo, Pam
APPLICANT: Bacobod, Jaime
APPLICANT: Stinchcomb, Dan
APPLICANT: Brochedo, Jaime
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
TITLE OF INVENTION: Lavels of Vascular Endothelial Growth Factor Receptor
CURRENT APPLICATION NUMBER: US 60/005,974
PRIOR FILING DATE: 1999-08-10
PRIOR FILING DATE: 1996-01-08
PRIOR FILING DATE: 1996-01-08
NUMBER OF SEQ ID NOS: 14225
SOFTWARE: PatentIn version 3.0
ENGYTHARE: PatentIn version 3.0
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                                                                                                                                                                           51.8%; Score 11.4; DB 4; Length 17; 69.2%; Pred. No. 2.3e+04; tive 3; Mismatches 1; Indels
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; Sequence 70.2, Application US/09401063
; Patent No. 6623952
; GENERAL INFORMATION:
APPLICANT: Akhtar, Saghir
APPLICANT: Pell, Patricia
; APPLICANT: McSwiggen, James
TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT
TITLE OF INVENTION: TO LEVELS OF EPIDERMAL GROWTH
; TITLE OF INVENTION: FACTOR RECEPTORS
NUMBER OF SEQUENCES: 1877
; CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 29
US-09-371-772B-4284
Sequence 4284, Application US/09371772B
; Patent No. 6566127
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STREET: 633 West Fifth Street
STREET: Suite 4700
       SOFTWARE: PatentIn version 3.0 SEQ ID NO 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 UGAUACAGGUAGA 15
                                                                                                                                                       Query Match
Best Local Similarity 69.2.
Best Local 9; Conservative
                                                                                                                                                                                                                                                                                                            4 TGTTACAGGTAGA 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-4284
                                                                                  ; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 9; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: U.S.A. ZIP: 90071-2066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 30
US-09-401-063-702
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                                                                                                                                                Score 11.4; DB 4; Length 17;
Pred. No. 2.3e+04;
4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                               Sequence 705, Application US/09401063

Sequence 705, Application US/09401063

Patent No. 6623862

GENERAL INFORMATION:
APPLICANT: Akhtar, Saghir
APPLICANT: Fell, Patricia
APPLICANT: Fell, Patricia
APPLICANT: McSwiggen, James
TITLE OF INVENTION: BIZYMATIC NUCLEIC ACID TREATMENT
TITLE OF INVENTION: OF DISBASES OR CONDITIONS RELATED
TITLE OF INVENTION: TO LEVELS OF EPIDERMAL GROWTH
TITLE OF INVENTION: FACTOR RECEPTORS
NUMBER OF SEQUENCES: 1877

CORRESPONDENCE ADDRESS:
ADDRESSE: Lyon & Lyon
STREET: Suite 4700

STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FRAELSC for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/401,063
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 230/107
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEPAA: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 705:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/985,162
FILING DATE: 04 December 1997
APPLICATION NUMBER: 60/036,476
FILING DATE: 31 January 1997
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
                                                                                                                                                         51.8%;
61.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 61.5%
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                                                                                                                                                    Query Match
Best Local Similarity 61.53
Matches 8; Conservative
                                                                                                                                                                                                                                            1 GCATGTTACAGGT 13
                                                                                                                                                                                                                                                                     3 GCAUUUUACAGGU 15
  SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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CITY: Los Angeles
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                                                                                          linear
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COUNTRY: U.S.A.
ZIP: 90071-2066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
US-09-401-063-705
                                                                                                              US-09-401-063-704
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                                                                                          TOPOLOGY:
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APPLICANT: Akhtar, Saghir
APPLICANT: Fell, Parricia
APPLICANT: MCSWiggen, James
TITLE OF INVENTION: FO DISEASES OR CONDITIONS RELATED
TITLE OF INVENTION: OF DISEASES OR CONDITIONS RELATED
TITLE OF INVENTION: FACTOR RECEPTORS
NUMBER OF SEQUENCES: 1877
CORRESPONDENCE ADDRESS:
ADDRESSER: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Galifornia
COUTTY: Los Angeles
STATE: California
COUTTY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                      Score 11.4; DB 4; Length 17; Pred. No. 2.3e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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COMPUTER READABLE FORM:
MEDIUM TYPE: 35" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
FILING DATE: 04 December 1997
APPLICATION NUMBER: 60/036,476
FILING DATE: 31 January 1997
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 320/107
TELECOMMUNICATION INFORMATION:
TELEPAN: (213) 955-0440
TELEPAN: (213) 955-0440
TELERAX: (7-3510
INFORMATION FOR SEQ ID NO: 703:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDENBES: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FSELSEG for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/401,063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PILING DATE:
CLASSIFICATION:
PROOF APPLICATION DATA:
APPLICATION NUMBER: 08/985,162
FILING DATE: 04 December 1997
APPLICATION NUMBER: 60/036,476
FILING DATE: 31 January 1997
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 230/107
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 32
US-09-401-063-704
; Sequence 704, Application US/09401063
; Patent No. 6623962
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INFORMATION FOR SEQ ID NO: 704:
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4 GCAUUUUACAGGU 16
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Best Local Similarity 61.5
Matches 8; Conservative
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TOPOLOGY:
US-09-401-063-703
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                                                                                      Query Match 51.8%; Score 11.4; DB 3; Length 18; Best Local Similarity 92.3%; Pred. No. 2.3e+04; Matches 12; Conservative 0; Mismatches 1; Indels
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; OTHER INFORMATION: sequences
US-09-531-000-34
                                                                                                                                                                                                                                                                                                                                                Sequence 7, Application US/09531000

Sequence 7, Application US/09531000

GENERAL INFORMATION:
APPLICANT: OGNISON, Marion D.
APPLICANT: JOHNSON, Marion D.
APPLICANT: JOHNSON, TRIPLEX IN-SITU HYBRIDIZATION
FILE REFERENCE: 2446-103
CURRENT APPLICATION NUMBER: US/09/531,000
CURRENT FILING DATE: 1996-11-10
PRIOR FILING DATE: 1996-11-10
PRIOR FILING DATE: 1996-11-10
PRIOR FILING DATE: 1997-11-10

PRIOR FILING DATE: 1997-11-10

NUMBER OF SEQ ID NOS: 77

SEQ ID NO 7

SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; GRNERAL INCORNATION:
; APPLICANT: JOHNSON, Marion D.
; APPLICANT: TOHNSON, Marion D.
; APPLICANT: FRESCO, Jacques R.
; TILLE OF INVENTION: TRIPLEX IN-SITU HYBRIDIZATION
; FILE REPERENCE: 2448-103
; CURRENT PILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: PCT/US98/23765
; PRIOR APPLICATION NUMBER: PCT/US98/23765
; PRIOR APPLICATION NUMBER: 1998-11-10
; PRIOR FILING DATE: 1998-11-10
; NUMBER OF SEQ ID NOS: 77
; SOPTWARE: PATENTIN VOS: 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 34, Application US/09531000; Patent No. 6461810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Artificial Sequence
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                          linear
STRANDEDNESS:
                       TOPOLOGY:
US-08-981-988A-27
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US-09-688-664B-79

Sequence 79, Application US/09685664B

Sequence 79, Application US/09685664B

Sequence 79, Application US/09685664B

Sequence 79, Application US/09685664B

Setent No. 681847

GENERAL INFORMATION:

APPLICANT: Pavco, Pam

APPLICANT: Stinctomb, Daime

APPLICANT: Scobedo, Jaime

TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Relate

TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Recptor

TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Recptor

CURRENT FILING DATE: 1995-10-26

PRIOR PILING DATE: 1995-10-26

PRIOR PILING DATE: 1995-01-08

PRIOR PILING DATE: 1995-01-08

PRIOR PILING DATE: 1995-01-08

PRIOR FILING DATE: 1995-01-08

PRIOR FILING DATE: 1995-01-08

NUMBER OF SED IN NOS: 8231

SOFTWARE: PatentIn version 3.0

SEQUING 79

LENGTH. 17
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ADDRESSE: VITTLE MALLYA SCIENTIFIC RESEARCH FOUNDATION
STREET: K. R. ROAD
CITY: BANGALORE
COINTY: INDIA
ZIP: 560 004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: PatentIn Release #1.0, Version #1.30 (EPO)
SOGTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51.8%; Score 11.4; DB 4; Length 17; 69.2%; Pred. No. 2.3e+04; tive 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Vittal Mallya Scientific Research Foundation
APPLICANT: The University of Leicester
TITLE OF INVENTION: Insulin
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9513967.1
FILING DATE: 08-JUL-1995
INFORMATION POR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 35
US-08-981-988A-27
; Sequence 27, Application US/08981988A
; Patent No. 6337194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 69.2-
Best Local 9; Conservative
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CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: RNA
ORGANISM: Homo sapiens
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US-08-882-046-89
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APPLICANT: Cohen. Daniel
APPLICANT: Chen. Daniel
APPLICANT: Chen. Daniel
APPLICANT: Chumakov, ilya
TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
FILE REPERENCE: GENSET.020CP1
CURRENT APPLICATION NUMBER: US/09/422,978
CURRENT APPLICATION NUMBER: US/09/422,978
EARLIER APPLICATION NUMBER: US 60/109,732
EARLIER FILING DATE: 1999-04-21
EARLIER FILING DATE: 1998-11-23
EARLIER PILING DATE: 1998-11-23
EARLIER PILING DATE: 1998-04-21
SERLIER PILING DATE: 1998-04-21
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; OTHER INFORMATION: upstream amplification primer 99-16772 for SEQ 2750,
US-09-422-978-6684
                                                         Gaps
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US-09-531-000-38
Score 11.4; DB 3; Length 19;
Pred. No. 2.3e+04;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51.8%; Score 11.4; DB 3; Length 19; 92.3%; Pred. No. 2.3e+04; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                           GEOUL 38

Sequence 38, Application US/09531000

Patent No. 6461810:
GENERAL INFORMATION:
APPLICANT: BACCHES R.
TITLE OF INVENTION: TRIPLEX IN-SITU HYBRIDIZATION
FILE REFERENCE: 2448-103
CURRENT APPLICATION NUMBER: US/09/531,000
CURRENT FILING DATE: 2000-09-08
PRIOR APPLICATION NUMBER: PCT/US98/23765
PRIOR APPLICATION NUMBER: PCT/US98/23765
PRIOR PILING DATE: 1998-11-10
PRIOR APPLICATION NUMBER: 1997-11-10
SOUTH APPLICATION NUMBER: 1997-11-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 6684, Application US/09422978
; Patent No. 6537751
     51.8%; 92.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                        8 ACAGGTAGAAAG 20
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Best Local Similarity 92.3
Matches 12; Conservative
  Query Match
Best Local Similarity 92.3
Matches 12; Conservative
                                                                                                             8 ACAGGTAGAAAG 20
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US-09-422-978-6684
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                                                                                                                                             Score 11.4; DB 4; Length 19; Pred. No. 2.3e+04;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRIE COMPUTER: U.C.

ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENT P. PC-DOS/MS-DOS
SOFTWARE: PATENTON DATA:
APPLICATION NUMBER: US-046
FILING DATE: 25-JUN-1997
CLASS/FICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: P-UW 2637
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-9001
TELEPHONE: CADABCTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
"WYD: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Campbell & Flores LLP
STREET: a 4370 La Jolla Village Drive, Suite 700
CITY: a 101ego
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
51.8%; Score 11.4; DB 3;
Best Local Similarity 92.3%; Pred. No. 2.4e+04;
Matches 12; Conservative 0; Mismatches 1;
                                  0; Mismatches
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   51.8%;
Query Match
Best Local Similarity 92.3°
Matches 12; Conservative
                                                                  8 ACAGGTAGAAAG 20
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                                                                                                   6 ACAGGAAGAAAG 18
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STRANDEDNESS: single
TOPOLOGY: linear
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188, App 80, Appl 12579, A 12580, A 177, App

us-09-743-825-7.max.rnpb

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Sequence 40680, A Sequence 9693, Ap Sequence 4522, Ap Sequence 4524, Ap Sequence 6072, Ap
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Sequence 12
Sequence 145
Sequence 145
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Sequence 145
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0. US-09-906-158-75
7. US-09-906-158-75
7. US-10-388-263-524
1. US-10-388-263-524
1. US-10-650-880-48
1. US-10-650-880-48
1. US-10-678-307-191
1. US-10-10-12580
2. US-10-831-901A-12580
2. US-10-831-901A-12580
2. US-10-831-901A-12580
2. US-10-831-901A-12580
2. US-10-831-901A-12593
3. US-10-922-626-197
3. US-10-922-969-101-72
3. US-10-922-969-101-72
3. US-10-922-340-454
3. US-10-922-340-454
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3. US-10-922-340-454
4. US-10-134-13-6672
5. US-10-922-340-117
5. US-10-922-340-12799
5. US-10-922-340-12799
6. US-10-922-901A-12799
6. US-10-922-901A-12799
6. US-10-931-901A-12799
6. US-10-751-736-31339
6. US-10-751
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50, Appl
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| cgn2_6/ptodata/2/pubpna/USO6_WAF.
| cgn2_6/ptodata/2/pubpna/USO6_WAF.
| cgn2_6/ptodata/2/pubpna/USO6_WAF. PUB.seq:*
| cgn2_6/ptodata/2/pubpna/USO6_PUBCOMB.seq:*
| cgn2_6/ptodata/2/pubpna/USO7_NEW_PUB.seq:*
| cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
| cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB
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                          GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-210-296-50
US-10-449-462-50
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US-09-988-681-157
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Maximum Match 100%
Listing first 100 summaries
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seq length: 22
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Perfect score:
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Searched:

Sequence:

15983, A

11, Appl 12, Appl 28206, A 28209, A 33372, A

12796, A 12797, A 12798, A

33372, A 117, App 4544, Ap 29, Appl 31, Appl 12578, A

14589,

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US-10-449-648-50

| Sequence 50, Application US/10449648 |
| Publication No. US20050143561A1 |
| GENERAL INFORMATION: |
| APPLICANT: Pfizer Products, Inc. |
| TITLE OF INVENTION: LAWSONIA INTRACELLULARIS PROTEINS AND RELATED METHODS AND |
| TITLE OF INVENTION: MATERIALS |
| FILE REFERENCE: 3153.00187/PC10589A |
| CURRENT APPLICATION NUMBER: US/10/449,648 |
| CURRENT PILING DATE: 2003-01-02 |
| PRIOR APPLICATION NUMBER: US/09/689,065B |
| PRIOR PLING DATE: 1999-11-2 |
| PRIOR PLING DATE: 1999-11-05 |
| PRIOR PLING DATE: 1999-11-05 |
| NUMBER OF SEQ ID NOS: 112 |
| SOFTWARE: PatentIn version 3.2 |
| LENGTH: 21 |
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US-10-449-462-50
is Sequence 50, Application US/10449462
is beduence 50, Application No. US2003020983A1
identity of US20030202983A1
identity of US20030202983A1
identity of INVENTION: LAWSONIA INTRACELLULARIS PROTEINS AND RELATED METHODS AND ITILE OF INVENTION: LAWSONIA INTRACELLULARIS PROTEINS AND RELATED METHODS AND ITILE OF INVENTION: MATERIALS
if TILE REFERENCE: 3153.00187/PC10589A
if CURRENT PRILING DATE: 2003-05-29
if PRIOR PLILING DATE: 2000-10-12
if PRIOR PLILING DATE: 1999-10-22
if PRIOR PLILING DATE: 1999-11-05
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                                                                                    60.0%; Score 13.2; DB 14;
83.3%; Pred. No. 1.7e+04;
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Pred. No. 1.7e+04;
0; Mismatches 3;
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; ORGANISM: Lawsonia intracellularis
US-10-449-462-50
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Best Local Similarity 83.3%;
Matches 15; Conservative
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Best Local Similarity
        US-10-210-296-50
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US-10-289-762-5333/c

US-10-289-762-5333/c

Sequence 5333, Application US/10289762

Publication No. US20040006218A1

GENERAL INFORMATION:

APPLICANT: GFITEAR: R.

TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevering the perference of infection of the perfection of the per
                                                                                                                      Sequence 79, Appl Sequence 4284, Ap Sequence 7261, Ap Sequence 79, Appl Sequence 7261, Ap Sequence 146, App Sequence 6684, Ap Sequence 6684, Ap Sequence 36, Appl Sequence 36, Appl Sequence 463, Appl Sequ
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36, Appl
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463, Appl
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Sequence 463, App
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Sequence 50, Application US/10210296

Publication No. US20030021802A1

GENERAL INFORMATION:
APPLICANT: Pfizer Products Inc.
TITLE OF INVENTION: LAWSONIA INTRACELLULARIS PROTEINS, AND RELATED
TITLE OF INVENTION: METHODS
TITLE OF INVENTION: AND MATERIALS
TITLE OF INVENTION NUMBER: US/10/206
CURRENT FILING DATE: 2002-09-01
PRIOR APPLICATION NUMBER: US/09/689,065
PRIOR APPLICATION NUMBER: US/09/689,065
NUMBER OF SEQ ID NOS: 102

SEQ ID NO 50

LENGTH: 21

LENGTH: 21
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US-09-848-754A-703
US-09-848-754A-705
US-09-848-754A-705
US-10-138-674-79
US-10-138-674-7261
US-10-138-674-7261
US-10-287-949A-7261
US-10-287-949A-7261
US-10-287-949A-7261
US-10-712-633-146
US-10-712-633-147
US-10-712-633-147
US-10-665-951-36
US-10-665-951-36
US-10-665-951-36
US-10-665-951-36
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US-10-665-951-36
US-10-665-951-36
US-10-758-155-36
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US-10-844-076-36
US-10-844-076-463
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ORGANISM: Lawsonia intracellularis
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; ORGANISM: Chlamydia pneumoniae
US-10-289-762-5333
        RESULT 2
US-10-210-296-50
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Gaps

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Indels

Length 19;

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ch 58.2%; Score 12.8; DB 10; 1 Similarity 87.5%; Pred. No. 2.6e+04; 14; Conservative 0; Mismatches 2;
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Best Local Similarity 87.5%;
Matches 14; Conservative
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                                                                                                        3 ATGTTACAGGTAGAAA 18
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US-09-988-686-157
                              Best Local Similarity
Matches 14; Conserv
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          Query Match
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### REPLICANT: Tavigian, Sean V.
### APPLICANT: Tavigian, Sean V.
### APPLICANT: Tavigian, Sean V.
### APPLICANT: Teng, David H.F.
### APPLICANT: Simard, Jodanna M.
### APPLICANT: Myriad Genetics, Inc.
### TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
### TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
### TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
### TITLE OF INVENTION: Gene and a Paralog
### PRIOR PELION NUMBER: US/09/98,626
### CURRENT APPLICATION NUMBER: US/09/98,626
### CURRENT PILING DATE: 2000-05-06
### PRIOR FILING DATE: 1998-11-06
### PRIOR FILING DATE: 1998-11-05
### NUMBER OF SEQ ID NOS: 240
### SEQ ID NOS: 240
### SEQ ID NO 157
### LENGTH: 19
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Publication No. US20030045704A1

GENERAL INFORMATION:

APPLICANT: Tavtigian, Sean V.

APPLICANT: Tavtigian, Bara V.

APPLICANT: Simard, Jacques

APPLICANT: Somens, Johanna M.

APPLICANT: Myriad Genetics, Inc.

TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility

TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes

FILE REFERENCE: 2318-258

CURRENT APPLICATION NUMBER: US/09/988,687

FRIOR APPLICATION NUMBER: US/09/564,805

PRIOR APPLICATION NUMBER: US 60/107,468

PRIOR APPLICATION NUMBER: US/09/434,382

PRIOR FILING DATE: 1998-11-05

NUMBER OF SEQ ID NOS: 240

SEQ ID NO 157

LENGTH: 19
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                                                                                                                                                                                                         Sequence 157, Application US/09988626
Publication No. US20030044959A1
                                      TGTTACAGGTAGAAAGC 21
                                                                                    2 regracaccaacaaaacc 19
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; ORGANISM: Homo sapiens
US-09-988-687-157
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; ORGANISM: Homo sapiens
US-09-988-626-157
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APPLICANT: Brett P. Monia
APPLICANT: Brett P. Monia
APPLICANT: Brett P. Monia
APPLICANT: Susan M. Freier
TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH FACTOR-BETA 3 EXPRESE
FILE REFERENCE: RTG-0257
CURRENT APPLICATION NUMBER: US/09/906,158
CURRENT FILING DATE: 2001-07-14
NUMBER OF SEQ ID NOS: 168
SEQ ID NO 75
LENGTH: 20
Sequence 157, Application US/09988686

Sequence 157, Application No. US20030120052A1

GENERAL INFORMATION:
APPLICANT: Tarvigian. Sean V.
APPLICANT: Tarvigian. Sean V.
APPLICANT: Tommens, Johanna M.
APPLICANT: Rommens, Johanna M.
APPLICANT: Myriad Genetics, Inc.
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
FILE REFERENCE: 2318-258
CURRENT FILING DATE: 2001-11-20
FRIOR FILING DATE: 1908-11-06
PRIOR FILING DATE: 1998-11-06
PRIOR FILING DATE: 1998-11-05
PRIOR FILING DATE: 1999-11-05
NUMBER OF SEQ ID NOS: 240
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 157
TENGTH. 10
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Pred. No. 2.6e+04;
n· Mismatches 2;
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; OTHER INFORMATION: Antisense Oligonucleotide
US-09-906-158-75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
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TYPE: DNA ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
                                                                      21 TTCTGGTAGAAAGCC 6
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Best Local Similarity
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; Publication No. US20030225528A1
; Sequence 220, Application No. US20030225528A1
; GENERAL INFORMATION:
; APPLICANT: BAKEY, Offere B. APPLICANT: Cronin, Maureen T. APPLICANT: Kiefer, Michael C. APPLICANT: Stak, Steve APPLICANT: Malker, Michael Graham
; TITLE OF INVENTION: GENE EXPRESSION PROFILING IN BIOPSIED TUMOR TISSUES
; TITLE OF INVENTION GENE EXPRESSION PROFILING IN BIOPSIED TUMOR TISSUES
; FILE REFERENCE: 39740-0001US
; CURRENT APPLICATION NUMBER: US 60/412,049
; PRIOR FILING DATE: 2002-09-18
; PRIOR FILING DATE: 2002-09-18
; PRIOR FILING DATE: 2002-09-18
; NUMBER OF SEQ ID NOS: 384
; SOFTWARE: FastERO for Windows Version 4.0
; SEQ ID NO 230
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APPLICANT: Cowsert, Lex M.
APPLICANT: Cowsert, Lex M.
APPLICANT: Baker, Brenda F.
APPLICANT: Sasmor, Henri M.
APPLICANT: Brookb. Douglas G.
APPLICANT: Brookb. Douglas G.
APPLICANT: Brookb. Douglas G.
APPLICANT: Brookb. Douglas G.
APPLICANT: Watt, Jacqueline R.
APPLICANT: Worlt, Jacqueline R.
APPLICANT: Worlt W.
APPLICANT: World W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Antisense Oligonucleotide US-10-388-263-524
                                                                                                                                                                       Sequence 524, Application US/10388263 Publication No. US20030228597A1
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18 TACAGGGAGAAAATCC 3
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Best Local Similarity 87.5
Matches 14; Conservative
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CRGANISM: Homo sapiens
US-10-388-360-230
                                                                                                                                                                                                                                             GENERAL INFORMATION:
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US-10-388-360-230/c
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Publication No. US20050014165A1

GENERAL INFORMATION:

APPLICANT: LEBE, NANCY M

TITLE OF INVENTION: BIOMARKER PANEL FOR COLORECTAL CANCER

FILE REFERENCE: CPMC-01000US1

CURRENT APPLICATION NUMBER: US/10/690,880

CURRENT FILING DATE: 2003-10-22

NUMBER OF SEQ ID NOS: 88

SOFTWARE: Patentin Ver: 2.1

SEQ ID NO 48
Sequence 191, Application US/10758307
; Sequence 191, Application US/10758307
; Publication No. US200402090A1
; GENERAL INFORMATION:
APPLICANT: GENOMIC HEALTH, INC.
; APPLICANT: RUSH UNIVERSITY MEDICAL CENTER
; APPLICANT: Cobleigh, Melody
APPLICANT: Shak, Steven
; APPLICANT: BAKer, Office
; APPLICANT: Cronin, Maureen
; TITLE OF INVENTION: GENE EXPRESSION MARKERS FOR BREAST
TITLE OF INVENTION: CANCER PROGNOSIS
; TITLE OF INVENTION: CANCER PROGNOSIS
; TITLE OF INVENTION: CANCER PROGNOSIS
; TITLE OF INVENTION WHERE: US/10/758,307
CURRENT FILING DATE: 2004-01-14
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 191
LEMOTH: 21
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Best Local Similarity 87.5%; Pred. No. 2.6e+04;
Matches 14; Conservative 0; Mismatches 2;
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Publication No. US20050064455A1

GENERAL INFORMATION:

APPLICANT: Genomic Health, Inc.

APPLICANT: Baker, Joffre

APPLICANT: Baker, Joffre

APPLICANT: Shak, Steven

APPLICANT: Shak, Steven

TITLE OF INVENTION: Gene Expression Markers for Predicting

TITLE OF INVENTION: Response to Chemotherapy

FILE REFERENCE: 39740-0010

CURRENT APPLICATION NUMBER: US/10/852,797

FILE REFERENCE: 3740-0010

CURRENT FILING DATE: 2003-05-28

NUMBER OF SEQ ID NOS: 372

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 80
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  Sequence 188. Application US/10714195
Publication No. US20050019785A1
GENERAL INFORMATION:
APPLICANT: Baker, Joffre
APPLICANT: Baker, Joffre
APPLICANT: Cronin, Maureen
APPLICANT: Shak, Steve
APPLICANT: Shak, Steve
TITLE OF INVENTION: POSITIVE CANCER
TITLE OF INVENTION: POSITIVE CANCER
TITLE OF INVENTION: POSITIVE CANCER
TILE REFERENCE: 39740-0005
CURRENT APPLICATION NUMBER: US/10/714,195
CURRENT APPLICATION NUMBER: 60/427090
PRIOR APPLICATION NUMBER: 60/427090
PRIOR FILING DATE: 2003-11-15
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ 1D NO 188
LIGHTH: 21
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ORGANISM: Artificial Sequence
FEATURE:
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US-10-714-195-188/C
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GREATLIANT CONSTITUTION US/10085A1
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APPLICANT: Haeboril, Peecer
APPLICANT: Haeboril, Peecer
APPLICANT: Haeboril, Peecer
TITLE OF INVENTION: Using Short Interference Mediated Inhibition of TRPM7 Gene Expression
TITLE OF INVENTION: Using Short Interfering Nucleic Acid (sinA)
FILE REFERENCE: 400/195 (MBHB04-535)
CURRENT APPLICATION NUMBER: US/10/883,218
CURRENT PILING DATE: 2004-07-013
PRIOR FILING DATE: 2004-07-013
PRIOR PELING DATE: 2004-04-16
PRIOR FILING DATE: 2004-04-16
PRIOR FILING DATE: 2004-01-14
PRIOR FILING DATE: 2004-01-14
PRIOR FILING DATE: 2004-01-14
PRIOR FILING DATE: 2003-10-23
PRIOR FILING DATE: 2003-10-23
PRIOR FILING DATE: 2003-10-23
PRIOR FILING DATE: 2003-10-23
PRIOR FILING DATE: 2003-4-30
PRIOR FILING DATE: 2003-4-30
PRIOR FILING DATE: 2003-4-30
PRIOR FILING DATE: 2003-6-20
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TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTOR POLYNUCLEOTIDES AND METHODS OF USE THE.
FILE REFERENCE: D0191 NP
CURRENT APPLICATION NUMBER: US/10/219,834
CURRENT FILING DATE: 2002-08-15
PRIOR APPLICATION NUMBER: US 60/313,658
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US-10-883-218-579
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   Length 19;
                                                                                  Indels
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Score 12.4; DB 22;
Pred. No. 4e+04;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 579, Application US/10883218 Publication No. US20050124567A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Sirna Therapeutics, Inc. APPLICANT: Haeberli, Peter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: RNA
ORGANISM: Artificial Sequence
   Query Match 56.4%;
Best Local Similarity 92.9%;
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 TTACAGGTAGAAA 19
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5 UUACAGCUAGAAAA 18
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Best Local Similarity
Matches 10; Conserv
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Squence 177 Application US/1088318

Publication No. US20050124567A1

GENERAL INPOMATION:

APPLICANT: Sirna Therapeuties, Inc.

APPLICANT: Sirna Therapeuties, Inc.

APPLICANT: Sirna Therapeuties, Inc.

APPLICANT: Sirna Therapeuties, Inc.

APPLICANT: MacSwiggen, James

TITLE OF INVENTION: USING Short Interfering Nucleic Acid (sina)

TITLE OF INVENTION: USING Short Interfering Nucleic Acid (sina)

TITLE OF INVENTION: USING Short Interfering Nucleic Acid (sina)

TITLE OF INVENTION: USING Short Interfering Nucleic Acid (sina)

TITLE OF INVENTION: USING Short Interfering Nucleic Acid (sina)

FRIOR PAPLICATION NUMBER: US 10/826,966

PRIOR PAPLICATION NUMBER: US 10/757,803

PRIOR PLILING DATE: 2003-05-24

PRIOR PLILING DATE: 2004-01-44

PRIOR PLILING DATE: 2003-11-24

PRIOR PLILING DATE: 2003-11-24

PRIOR PLILING DATE: 2003-05-23

PRIOR APPLICATION NUMBER: US 10/444,853

PRIOR PLILING DATE: 2003-05-23

PRIOR PLILING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57.3%; Score 12.6; DB 21;
78.9%; Pred. No. 3.2e+04;
tive 0; Mismatches 4;
   PRIOR APPLICATION NUMBER: 60/468,562
PRIOR FILING DATE: 2003-05-06
PRIOR PILING DATE: 2003-06-06
PRIOR PILING DATE: 2003-06-06
PRIOR PILING DATE: 2003-06-06
PRIOR PILING DATE: 2003-05-06
PRIOR APPLICATION NUMBER: 60/468,627
PRIOR PILING DATE: 2003-06-07
PRIOR PILING DATE: 2003-06-10
PRIOR FILING DATE: 2003-06-10
PRIOR FILING DATE: 2003-06-17
NUMBER OF SEQ ID NOS: 30063
SOFTWARE: PREUSED FOR WINDOWS VERSION 4.0
SOFTWARE: PASCED FOR WINDOWS VERSION 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Antisense compound US-10-831-901A-12580
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Best Local Similarity 78.9
Matches 15, Conservative
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US-10-883-218-177/c
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; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/sinA sense r
US-10-922-626-197
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APPLICANT: SITMA THEAPQUICES
APPLICANT: Guerciclini, Roberto
APPLICANT: Guerciclini, Roberto
APPLICANT: McSwiggen, James
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Angiopoietin Gene
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Angiopoietin Gene
TITLE OF INVENTION: RAPPLICATION NUMBER: US/10/922,626
CURRENT FILING DATE: 2004-08-24
PRIOR FILING DATE: 2004-08-24
PRIOR FILING DATE: 2004-04-16
PRIOR FILING DATE: 2004-04-30
PRIOR FILING DATE: 2004-04-30
PRIOR FILING DATE: 2004-04-30
PRIOR FILING DATE: 2004-05-13
PRIOR FILING DATE: 2001-05-18
PRIOR FILING DATE: 2001-05-18
PRIOR FILING DATE: 2001-05-18
PRIOR FILING DATE: 2001-05-30-66
PRIOR FILING DATE: 2001-05-30-66
PRIOR FILING DATE: 2001-05-30-66
PRIOR FILING DATE: 2001-05-30-66
PRIOR FILING DATE: 2001-07-20
PRIOR FILING DATE: 2001-07-20
PRIOR FILING DATE: 2001-07-30-66
PRIOR FILING DATE: 2001-07-20
PRIOR FILING DATE: 2001-07-30-66
PRIOR 
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; OTHER INFORMATION: upstream amplification primer 99-17762 for SEQ 845,
US-10-349-143-4779
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                                PRIOR APPLICATION WINBER: EARLIER APPLICATION NUMBER: US 60/109,732
PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
PRIOR PILING DATE: BARLIER FILING DATE: 1998-04-21
NUMBER OF SEQ ID NOS: 11796
SEQ ID NO 4779
LENGTH: 18
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Best Local Similarity 82.4%; Pred. No. 5.1e+04;
Matches 14; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 12.2; DB 17;
Pred. No. 5e+04;
0; Mismatches 3;
PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-922-626-197/c
; Sequence 197, Application US/10922626
; Publication No. US20050159380A1
; GENERAL INFORMATION:
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ilarity 82.4%;
Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Sirna Theraputics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity F
                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo Sapiens
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                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
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Sequence 92, Application US/10436715
Sequence 92, Application US/10436715
Sequence 92, Application US/10436715
Sequence 92, Application On US20040018976A1
Sequence 92, Application No. US20040018976A1
GENERAL INFORMATION:
TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING NOVEL HUMAN G-PROTEIN COUPLED RECEPTORS, TITLE OF INVENTION: AND SPLICE VARIANTS THEREOF
FILE REFERENCE: D0262 NP
CURRENT FILING DATE: 2003-05-13
PRIOR APPLICATION NUMBER: U.S. 60/380,336
PRIOR FILING DATE: 2002-05-14
NUMBER OF SEQ ID NOS: 471
SOFTWARE: Patentin version 3.2
SEQ ID NO 92
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Publication No. US20040005584A1
Publication No. US20040005584A1
Publication No. US20040005584A1
Publication No. US20040005584A1
APPLICANT: Cohen, Daniel
APPLICANT: Chumakov, Ilya
APPLICANT: Chumakov, Ilya
TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
FILE REFERENCE: GENSET.020CP1
CURRENT APPLICATION NUMBER: US/10/349,143
FURNE APPLICATION NUMBER: US/99/422,978
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
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Pred. No. 4.1e+04;
0; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 12.4; DB 14; Length 20;
Pred. No. 4.1e+04;
0; Mismatches 1; Indels (
                                         PRIOR FILING DATE: 2001-10-30
PRIOR FILING DATE: 2001-10-30
PRIOR FILING DATE: 2001-10-30
PRIOR APPLICATION NUMBER: US 60/318,675
PRIOR FILING DATE: 2001-09-12
PRIOR FILING DATE: 2002-02-06
PRIOR FILING DATE: 2002-02-06
PRIOR FILING DATE: 2001-11-26
PRIOR FILING DATE: 2001-11-26
PRIOR FILING DATE: 2001-11-26
PRIOR FILING DATE: 2001-11-36
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92.9%;
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Best Local Similarity 92.37
The state of the 
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Best Local Similarity 92.9'
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CORGANISM: Homo sapiens
US-10-436-715-92
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ORGANISM: Homo sapiens
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US-10-349-143-4779
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Query Match
Best Local Similarity
Matches 14; Conserva
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US-09-888-361-50
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LENGTH: 20
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APPLICANT: Sirna Theraputies
APPLICANT: Guerciolini, Roberto
APPLICANT: Guerciolini, Roberto
APPLICANT: Guerciolini, Roberto
APPLICANT: Guerciolini, Roberto
APPLICANT: Guerciolini, Septemble Company Co
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APPLICANT: C. Frank Bennett
APPLICANT: Robert Rothlein
APPLICANT: Takashi Kei Kishimoto
APPLICANT: Takashi Kei Kishimoto
APPLICANT: Lex M. Cowsert
TILE OF INVENTION: ANTISENSE MODULATION OF TALIN EXPRESSION
FILE REPERENCE: RTS-0099
CURRENT APPLICATION NUMBER: US/09/791,942
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 89
SEQ ID NO 44
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Best Local Similarity 70.6%; Pred. No. 5.1e+04;
Matches 12; Conservative 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                ; Sequence 438, Application US/10922626; Publication No. US20050159380A1; GENERAL INFORMATION:
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Patent No. US20020147166A1
GENERAL INFORMATION:
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                                             TTACAGGCAGAGAAGAC 3
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Sequence 50, Application US/0988361
Publication No. US20030064944A1
GENERAL INFORMATION:
TITLE OF INVENTION: BEPRESSION
FILE REFERENCE: RTS-0158
CURRENT APPLICATION NUMBER: US/09/888,361
CURRENT FILING DATE: 2001-06-21
NUMBER OF SEQ ID NOS: 163
ENGINE: 20
LENGTH: 20
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APPLICANT: C. Frank Bennett
APPLICANT: C. Frank Bennett
APPLICANT: C. Frank Bennett
TITLE OF INVENTION: ANTISENSE MODULATION OF TALIN EXPRESSION
FILE REPERENCE: RTSP-0198
CURRENT APPLICATION NUMBER: US/10/415,463
CURRENT FILING DATE: 2003-11-13
PRIOR APPLICATION NUMBER: 09/702,251
PRIOR FILING DATE: 2000-10-30
NUMBER OF SEQ ID NOS: 89
SEQ ID NO 44
LENGTH: 20
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                                                                                                                                     55.5%; Score 12.2; DB 9; Length 20; 82.4%; Pred. No. 5.1e+04; Live 0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55.5%; Score 12.2; DB 10;
illarity 82.4%; Pred. No. 5.1e+04;
Conservative 0; Mismatches 3;
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                                                                OTHER INFORMATION: Antisense Oligonucleotide
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; Sequence 44, Application US/10415463
; Publication No. US20040110705A1
; GENERAL INFORMATION:
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TYPE: DNA ORGANISM: Artificial Sequence FEATURE:
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Best Local Similarity 82.45
Matches 14; Conservative
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RESULT 31
US-10-751-736-831/c
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Pred. No. 5.1e+04;
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APPLICANT: Bennett, C. Frank
APPLICANT: Dobie, Kenneth W.
APPLICANT: Dobie, Kenneth W.
APPLICANT: Dobie, Kenneth W.
APPLICANT: Dobie, Review C.
TITLE OF INVENTION: MODULATION OF CEACAMI EXPRESSION
TITLE OF INVENTION: MODULATION OF CEACAMI EXPRESSION
CURRENT APPLICATION NUMBER: 105/10/101
CURRENT FILING DATE: 2004-07-12
PRIOR FILING DATE: 2003-07-12
NUMBER OF SEQ ID NOS: 298
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 20
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; Publication No. US20050107324A1
; GENERAL INFORMATION:
   APPLICANT: Bennett, C. Frank
; APPLICANT: Dobie, Kenneth W.
; TITLE OF INVENTION: MODULATION OF CEACAMI EXI
   TITLE FERENCE: ISISO101-100 (RTS-0655US)
; CURRENT FILING DATE: 2004-07-12
; PRIOR PILING DATE: 2004-07-12
; RUMBER OF SEQ ID NOS: 298
; SOFTWARE: FASESEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 50, Application US/10705715 ; Publication No. US20040147472A1
                                                                                    RESULT 27
US-10-889-101-72
; Sequence 72, Application US/10889101
; Publication No. US20050107324A1
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TGTTACAGGTAGAAAG 20
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82.4%;
                      TGTTGCAGGCAGCAAAG 3
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Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 82.4
Matches 14; Conservative
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CORGANISM: H. sapiens
US-10-889-101-218
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US-10-889-101-218/c
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US-10-705-715-50
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LENGTH: 20
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APPLICANT: Jacqueline Wyatt
TITLE OF INVENTION: EXPRESSION
FITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH FACTOR BETA RECEPTOR
FITLE OF INVENTION: EXPRESSION
FILLE REFERENCE: RTS-0158
CURRENT APPLICATION NUMBER: US/10/705,715
CURRENT APPLICATION NUMBER: US/90/888,361
PRIOR APPLICATION NUMBER: US/99/888,361
PRIOR FILING DATE: 2001-06-21
SEQ ID NOS: 163
LENGTH: 20
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APPLICANT: Brown, Eugene
APPLICANT: Liu, Wei, Wei
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON
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LOCATION: 1..21
OTHER INFORMATION: upstream amplification primer 99-44259 for SEQ 103,
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TITLE OF INVENTION: Obesity Associated Biallelic Marker Maps
FILE REPERENCE G-083US02PCT
CURRENT APPLICATION NUMBER: US/10/333,429
CURRENT FILING DATE: 2003-01-17
FRIOR APPLICATION NUMBER: PCT/IB01/01477
FRIOR APPLICATION NUMBER: US 60/219,704
FRIOR FILING DATE: 2000-06-28
FRIOR FILING DATE: 2000-07-18
FRIOR FILING DATE: 2001-06-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 20;
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82.4%; Pred. No. 5.1e+04;
tive 0; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Antisense Oligonucleotide US-10-705-715-50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 274, Application US/10333429; Publication No. US20040048265A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 831, Application US/10751736
; Publication No. US20040265230A1
; GENERAL INFORMATION:
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Best Local Similarity 82.4
Matches 14; Conservative
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Sequence 15982, Application US/10751736, Publication No. US20040265230A1 GENERAL INFORMATION:
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SOFTWARE: PatentIn version 3.2
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Best Local Similarity 82.4%;
Matches 14; Conservative (
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Best Local Similarity 64.7
Matches 11; Conservative
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US-10-751-736-15982
                                                             ; TYPE: RNA
; ORGANISM: RNAi
US-10-751-736-10500
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US-10-751-736-15983
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; ORGANISM: RNAi
US-10-751-736-15983
                     SEQ ID NO 10500; LENGTH: 21
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Publication No. US20040265230A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Watth
APPLICANT: Martinez, Robert
APPLICANT: Liu, Weith
APPLICANT: Liu, Weith
APPLICANT: AND METHODS FOR DIAGNOSING AND TREATING COLON
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON
CURRENT APPLICATION NUMBER: US/10/751,736
CURRENT FILING DATE: 2003-01-06
PRIOR APPLICATION NUMBER: US Provisional Application 60/438,000
PRIOR FILING DATE: 2003-01-06
NUMBER OF SEQ ID NOS: 54873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Wyeth
APPLICANT: Martinez, Robert
APPLICANT: Martinez, Robert
APPLICANT: Martinez, Robert
APPLICANT: Brown, Eugene
APPLICANT: Liu, Wei
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON
TITLE OF INVENTION: CANCERS
FILE REFERENCE: AM100927 (031896-002000)
CURRENT APPLICATION NUMBER: US/10/751,736
CURRENT FILING DATE: 2003-01-06
PRIOR PILING DATE: 2003-01-06
NUMBER OF SEQ ID NOS: 54873
SOFTWARE: PATENTIN Version 3.2
SEQ ID NO 1680
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            FILE REFERENCE: AMIO0227 (031896-002000)
CURRENT APPLICATION NUMBER: US/10/751,736
CURRENT FILING DATE: 2003-01-06
RIOR APPLICATION NUMBER: US Provisional Application 60/438,000
PRIOR FILING DATE: 2003-01-06
NUMBER OF SEQ ID NOS: 54873
SEQ ID NO 831
LENGTH: 21
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Pred. No. 5.1e+04;
0; Mismatches 3;
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Pred. No. 5.1e+04;
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82.4%;
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                                                                                                                                                                                                                                                                                                          Similarity
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                                                                                                                                                                                                       ; TYPE: RNA
; ORGANISM: RNAi
US-10-751-736-831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: RNA
ORGANISM: RNAi
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Best Local
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Sequence 15983, Application US/10751736
; Publication No. US20040265230A1
; GENERAL INFORMATION:
    GENERAL INFORMATION:
    APPLICANT: Wattinez, Robert
    APPLICANT: Brown, Eugene
    APPLICANT: Liu, Wei
    TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON
    TITLE OF INVENTION: CANCERS
    TITLE OF INVENTION: CANCERS
    TITLE OF INVENTION: USAGE: US/10/751,736
    CURRENT FILING DATE: 2003-01-06
    PRIOR FILING DATE: 2003-01-06
    NUMBER OF SEQ ID NOS: 54873
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 15983
    LENGTH: Liu
                                                                                                                                                                                                                                                                                                                                 APPLICANT: Wyeth
APPLICANT: Wattinez, Robert
APPLICANT: Brown, Eugene
APPLICANT: Brown, Eugene
APPLICANT: Liu, Wei Gompositions and Methods For Diadrosing and Treating Colon
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON
TITLE OF INVENTION: CANCERS
FILE REFERENCE: AMINOS27 (031896-002000)
CURRENT APPLICATION NUMBER: US/10/751,736
CURRENT PILING DATE: 2003-01-06
PRIOR PILING DATE: 2003-01-06
NUMBER OF SEQ ID NOS: 54873
SOFTWARE: Patentin version 3.2
LENGTH: 21
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  Length 21;
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                                                  Indels
55.5%; Score 12.2; DB 20; 64.7%; Pred. No. 5.1e+04; ive 3; Mismatches 3;
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Pred. No. 5.1e+04;
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GENERAL INFORMATION:
APPLICANT: Effertz, Roger J.
APPLICANT: Effertz, Roger J.
TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping
FILE REFERENCE: 38-10(52679)A
CURRENT APPLICATION NUMBER: US/09/969,373
CURRENT FILING DATE: 2001-10-02
PRIOR FILING DATE: 2001-01-05
PRIOR FILING DATE: 2001-01-05
PRIOR APPLICATION NUMBER: US 09/750,427
PRIOR FILING DATE: 2001-01-13
PRIOR FILING DATE: 2001-01-13
PRIOR FILING DATE: 2001-05-15
NUMBER OF SEQ ID NOS: 4593
SEQ ID NO 4224
                                                                                                                                                                                                                                                                                                Sequence 4522, Application US/09969373
Fatent No. US2002013892A1
GENERAL INFORMATION:
APPLICANT: Effertz, Roger J.
APPLICANT: Effertz, Roger J.
TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping
FILE REFERENCE: 38-10(52579) A
CURRENT FILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: US 09/754,853
PRIOR APPLICATION NUMBER: US 09/760,427
PRIOR APPLICATION NUMBER: US 09/760,427
PRIOR APPLICATION NUMBER: US 09/760,427
PRIOR PILING DATE: 2001-01-13
PRIOR PILING DATE: 2001-01-13
FRIOR PRILING DATE: 2001-01-13
FRIOR PILING DATE: 2001-05-15
NUMBER OF SEQ ID NOS: 4593
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Pred. No. 7.9e+04;
0; Mismatches 2; Indels
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54.5%; Score 12; DB 17; Length 20; 75.0%; Pred. No. 6.4e+04;
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           6.4e+04;
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Pred. No. 7.9e+04;
); Mismatches 2;
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86.7%;
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Best Local Similarity 86.7%
13; Conservative
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Best Local Similarity 86.7
Matches 13; Conservative
                                                                Conservative
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                                Best Local Similarity
Matches 15; Conserv
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           Query Match
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US-10-349-143-9693/C
Sequence 9693, Application US/10349143
Sequence 9693, Application US/10349143
Sequence 9693, Application US/20040005584A1
GENERAL INFORMATION:
Sequence 9693, Application US/20040005584A1
GENERAL INFORMATION:
Sequence 9693, Application US/2004005584A1
GENERAL INFORMATION:
Sequence 9693, Application US/20040051
SETION PROPERTION:
SETION SEQUENCE:
SETION SEQUENCE:
SETION OF SEQUENCE:

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LOCATION: 1...20

1 OTHER 110-149-143-9693

US-10-349-143-9693
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APPLICANT: Liu, Wei
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON
TITLE OF INVENTION: CANCERS
FILE REPERENCE: AM100927 (031896-002000)
CURRENT APPLICATION NUMBER: US/10/751,736
CURRENT FILING DATE: 2003-01-06
PRIOR PPLICATION NUMBER: US Provisional Application 60/438,000
PRIOR PILING DATE: 2003-01-06
NUMBER OF SEQ ID NOS: 54873
SOFTWARE: Patentin version 3.2
SEQ ID NO 40680
LENGTH: 21
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Pred. No. 5.1e+04;
0; Mismatches 3; Indels (
           Length 21;
                                                                   Indels
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     Query Match 55.5%; Score 12.2; DB 20; Best Local Similarity 70.6%; Pred. No. 5.1e+04; Matches 12; Conservative 2; Mismatches 3;
                                                                                                                                                                                                                                                                                                                     Sequence 40680, Application US/10751736
Publication No. US20040265230A1
GENERAL INFORMATION:
                                                                                                                        1 GCATGTTACAGGTAGAA 17
                                                                                                                                                            1 GCAUGUCACUGGAAGAA 17
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82.4%;
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Best Local Similarity
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ORGANISM: RNAi
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## Sequence 6072, Application US/10349143

## SPLICANT: Cohen, Daniel

## APPLICANT: Blumenfeld, Marta

## APPLICANT: Chumakcov, Ilya

## TITLE OF INVENTION: Biallelic markers for use in constructing a high density...

## TITLE OF INVENTION: Biallelic markers for use in constructing a high density...

## TITLE OF INVENTION: Biallelic markers for use in constructing a high density...

## CURRENT PLING DATE: 2003-01-21

## PRIOR FILING DATE: 1999-10-20

## PRIOR PELING DATE: 1999-10-20

## PRIOR PELING DATE: EARLIER FILING DATE: 1999-04-21

## PRIOR PILING DATE: EARLIER FILING DATE: 1998-04-21

## PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21

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## PRIOR FILING DATE: DATE: DATE: 1998-04-21

## PRIOR FILING DATE: DATE: DATE: DATE: 1998-04-21
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NAMEKEY: primer_bind
LOCATION: 1.13
COTHER INFORMATION: upstream amplification primer 99-8748 for SEQ 2138,
US-10-349-143-6072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 53.6%; Score 11.8; DB 17; Length 19; Best Local Similarity 86.7%; Pred. No. 7.9e+04; Matches 13; Conservative 0; Mismatches 2; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo Sapiens
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1 Grragaggrrgaaa 15 셤

5 GTTACAGGTAGAAA 19

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Gaps

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Search completed: August 12, 2005, 10:02:51 Job time : 373 secs

AZ786362 2M0031N16 CL668834 PRI0158d AZ396022 1M0160J20 AZ787298 2M0033016 CL687844 PRI0147d AG197947 Pan trogI AZ312945 1M0029P03 AZ774536 2M004P01 AJ796099 AZ428984 1M0212P03	A2942905 2M0203K13 A4459970 T. brucei CO78447 BLO09D A0 AZ612157 BLO09D A0 AZ612157 LM0438L21 AZ817291 ZM0086P05 AU008312 AU008312 AZ348213 1M0084N15 AZ348213 1M0084N15 AZ35874 1M0053N15 AZ357874 1M0059D13 AZ807992 ZM0071C14 AJ590809 Arabidops AL488091 T. brucei CL670376 PRIO161d CL670376 PRIO161d CR295672 3M07-c07-K AZ865832 ZM0176D09 AU256704 AU256704 D18242 MUGGS00522 AZ32875 1M0052A01	AZ489135 1M0319H15 AZ489135 1M0337F19 AZ78233 2M002101 AZ345854 1M0080F16 AW250981 2822267.3 BQ789814 hage002aF AZ328922 1M0059D23 AZ358367 1M0390D06 AZ368367 1M0390D06 AZ36817 1M0119A16 AZ462631 1M0269F12 AZ490568 1M0230B07 AZ490560 1M0230B07 AZ490560 1M0230B07 AZ490560 1M0230B07 AZ490560 1M0520B07 AZ490560 1M0520B07 AZ49056 2M00323B07 BX553324 AZ43980 1M0563A05 AZ59800 1M0412F01 AZ59800 1M0412F01 AZ59800 1M0563A05 AZ776420 2M0016022	AZ501345 1M0340111 AZ510074 1M0345111 AZ8190555 ZM0274N14 CZ1103 HUMGS000262 AZ59163 1M0461M13 AZ523493 1M0461M13 AZ508068 1M0010N08 AZ407755 1M0178E04 AZ77208 1M0574P11 AU257209 AU257209 AZ40257209 1M0574P11 AU257209 AU257209 AZ41444 1M0169A15 AZ51444 1M0169A15 AZ514827 HD-03-10 AZ824702 ZM00399P20 AZ51990 Arabidops CL683179 PRI0136a AZ597767 1M0412C22 AZ593765 1M0162M07
∞ 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	3 日 日 日 日 日 日 日 日 日 日 日 日 日 日 日 日 日 日 日		22 8 AZ501345 22 8 AZ501345 22 8 AZ501345 22 8 AZ510551 22 8 AZ590555 17 6 C21103 20 8 AZ23493 20 8 AZ23493 20 8 AZ23493 21 1 AZ52499 21 1 AZ52499 21 1 AZ52499 21 8 AZ407675 22 1 AZ510899 21 8 AZ514444 22 1 AZ519627 22 8 AZ519627 23 8 AZ624109 24 8 AZ624109 25 8 AZ624109 26 8 AZ624109 27 CF314827 28 AZ624102 29 AJ589581 20 8 AZ637615 20 8 AZ637615 21 9 AJ589581 22 8 AZ637615 23 8 AZ637615 24 8 AZ637615 25 8 AZ637767
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GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd. leic search, using sw model August 12, 2005, 05:54:16; Search time 1779 Second the Second S	470.722 143-825-7 1ttacaggtagaaaagcc 22 1.0.0 , Gapext 1.0 14 seqs, 19032134700 residue 1tisfying chosen parameters: 0 22 22 22 22 22 22 22 22 22 22 22 22 2	b_est1:* b_est2:* b_hest3:* b_est3:* b_est4:* b_est5:* b_est6:* b_est6:* b_est6:* b_est6:* b_est6:* b_est6:* b_ast8:* b_	2.7 22 8 AZ659094 0.0 20 9 TA559F10Q 0.0 20 8 AZ452265 9.1 20 9 CL681335 8.2 20 8 AZ775974 8.2 20 8 AZ775974 8.3 22 8 AZ775974 6.4 21 9 CL436392 6.4 21 8 AZ649514 5.5 20 1 AUG08116 5.5 20 1 AUG08116 5.5 20 8 AZ78233 6.5 21 8 AZ828233 6.5 21 8 AZ828233 6.5 21 8 AZ828233 6.5 20 8 AZ77971 6.5 20 8 AZ77971 6.5 20 8 AZ787974 6.5 20 8 AZ782409 6.5 20 9 AZ782409 6.5 21 8 AZ843033 6.5 20 9 AZ782409 6.5 20 9 AZ7828409 6.5 20 9 AZ7828409
Co OM nucleic - nucleic Run on: Augu	Title: Perfect score: 22 Sequence: 1 gcatg Scoring table: IDENTIT Gapop 1 Searched: 3423954 Total number of hits 86 Minimum DB seq length: Maximum DB seq length: Maximum DB seq length: Maximum DB seq length: Maximum DB seq length:	Database : EST: 1: 9 3: 9 3: 9 4: 9 6: 9 7: 9 7: 9 8: 9 9: 9 Pred. No. is th Score greater t and is derived Regult No. Score Match	2 2 2 2 2 3 4 4 4 4 4 4 4 4 4 4 4 4 4 4

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nhi@sanger.ac.uk
Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
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                                                                                                                                                                                                                                                                       TA359F10Q 20 bp DNA linear GSS 13-DEC-2000 T. brucei sheared genomic DNA clone 359f10, reverse sequence, genomic survey sequence.
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Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Melville, S. E., Rajandream, M.A. and Barrell, B.G.
Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 18A, B-mail: barrell@sanger.ac.uk and
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
1 (bases 1 to 20)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
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Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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88.2%; Pred. No. 5.3e+04;
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/strain="TREU927"
/db_xref="taxon:5691"
/clone="359f10"
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                                                                                                                                                6 ATGATACAGGTAGTAAA 22
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                       Similarity 88.2
15; Conservative
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/ Jab host="E. Coli strain XLI0-Gold, T1-resistant, F-"
/ Clool 1bb-"Mouse 10kb plasmid UUGCIM library.
/ Clool 1bb-"Mouse 10kb plasmid UUGCIM library.
/ Inde="Vector: PWAJATV; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynuclectide kinase. Adaptor oligonuclectides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMDA2 (ggl 4732114)gbl AR129072.1); a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XLI0-Gold (Stratagene) cells
and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. Bammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 22)

S Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacce,S., Mahmoud,M., Menen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R., Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

L Unpublished (2000)

Contact: Robert B. Weiss
University of Utah

Duniversity of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
                                                                                                                                                                                                                                                                               GSS 14-DEC-2000
                                                                                                                                                                                                                                                                          AZ659094 140536E16F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0536E16 F, genomic survey sequence.
                         AZ788165 2M0035P02
AU254575 AU254575
AZ331643 1M0059P12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0536 row: E column: 16
Seg primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
                                                                                                                                                      ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C578L/63"
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clone="UUGC1M0536E16"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   High quality sequence stop: 22.
Location/Qualifiers
                         AZ788165
AU254575
AZ331643
                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (house mouse)
Mus musculus
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                               ∞ ⊢ ∞
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Fax: 801 585 7177
Email: ddunn@genet
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Query Match

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COMMENT

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AZ651001 100521023F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0521023 F, genomic survey sequence.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (Dass 1 to 22)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weise, R.,

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts
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84112, USA
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Srinivasan, J., Otto, G.W., Kahlow, U., Geisler, R. and Sommer, R.J. AppabB: an AcedB database for the nematode satellite organism Pristionchus pacificus
Nucleic Acids Res. 32 (1), D421-D422 (2004)
                                                                                                                                                                              Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Max-Planck-Institute for Developmental Biology
Max-Planck-Institute for Developmental
Tel: 00497071601371
Fax: 00497071601498
Fax: 0049707
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
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Pred. No. 1.5e+06;
0; Mismatches 2;
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Insert Length: 10000 Std Error: 0.00
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Seg primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
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/organism="Mus musculus"
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/strain="C57BL/6J"
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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Location/Qualifiers
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Best Local Similarity 85.7
Matches 12; Conservative
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Fax: 801 585 7177
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                 AUTHORS
                                                                                                                     JOURNAL
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          Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Waiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
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PRIO130d B07 2 - PRIO130d.BR (20) Note: Recurring String Mixed stage fosmid library of P. pacificus var. California Pristionchus pacificus genomic, genomic survey sequence.
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/clone lib="Mouse 10kb plasmid UGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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Neodiplogasteridae; Pristionchus.
1 (bases 1 to 20)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0252 row: H column: 06
Seq primer: CGTTGTAAAACGACGACCAGT
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/mol_type="genomic DNA"
/strain="C578L/63"
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clone="UUGC1M0252H06"
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High quality sequence stop: 20.
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                                                                                                                                                                                                                                                                                                                                                                                            Tel: 801 585 5606
Fax: 801 585 7177
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13 ACAGGTAGAAA 3
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Laboratory Mouse DNA Resource Laboratory Mouse DNA Resources (documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. Coli XII0-Gold (Stratagene) cells and selected for ampicillin resistance."
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U3NeoSV1 gene trap. Tag generated by plasmid rescue. Additional
sequence information and target gene cloning can be generated. ES
cell line harboring insertion mutation of target gene is available.
Sequence analysis available from
http://140.193.242.7/esdb/public_search_frame.php?PST=PST2884-NL.Se
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1. (bages 1 to 21)
                                                                              /lab_host="B. Coli strain XL10-Gold, T1-resistant, F-"
/clome l1b="Mouse 10kb plasmid UUGCM library"
/note="Voctor: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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Manitoba Institute of Cell Biology, Universitry of Manitoba
ONS029, 675 McDermot Ave, Winnipeg, MB R3E 0V9, Canada
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/clone="PST2884-NL.Seg"
/db_xref="taxon:10090"
/clone="UUGC2M0009H14"
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Unpublished (2002)
Contact: Hicks GG
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Fax: 204 787 2190
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Class: Gene Trap.
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Best Local Similarity
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CL436392
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                                                                                                                                                                                                                 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwalot (gilly 4732114 [gb] AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chamically-competent B. coli Xii0-Gold (Stratagene) cells and selected for ampicillin resistance."
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Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.

E 1 (bases 1 to 20)

S Dunn, D., Aoyaqi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.,
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah Genome Center
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                                                                                 /lab_host="E. Coli strain XLIO-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UTGCIM library"
/note="Vector: PWD42rv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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Pred. No. 1.5e+06;
0; Mismatches 2; Indels
                                                                                                                                                                                                      Laboratory Mouse DNA Resource
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/mol_type="genomic DNA"
/strain="C57BL/6J"
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Class: plasmid ends
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  /db_xref="taxon:10090"
/clone="UUGC1M0521023"
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Fax: 801 585 7177
Email: ddunn@geneti
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Best Local Similarity 85.77
Matches 12; Conservative
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AZ649514/c
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/ Jab host="E" coli strain XL10-Gold, T1-resistant, F-"
/ clone lib="Mouse 10kb plasmid UUGC2M library"
/ clone lib="Mouse 10kb plasmid UUGC2M library"
/ note="Vector: PWD42nv; Purified genomic DNA from M.
musculus G57BL/GJ (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymuclectide kinase. Adaptor oligonuclectides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
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2M0274N14F Mouse 10kb plasmid UUGC2M library Mus musculus genomic
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Mus musculus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Bumalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 22)

Bunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,

Reilly,M., Rose,M., Sond Wright,D.,Weiss,R., Tingey,A., von

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts
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                                                                                                                                                            ch 48.2%; Score 10.6; DB 9; Length 21; 1 Similarity 76.5%; Pred. No. 1.9e+06; 13; Conservative 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           clone UUGC2M0274N14 F, genomic survey sequence.
/cell_type="Embryonic stem cell"
/cell_line="D3H (J1 subclone)"
/clone_lib="MICB1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0274 row: N column: 14
Seg primer: CGTYCTAAAACGACGGCCAGT
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/mol_type="genomic DNA"
fetrain="C57BL/6"
/db_xref="taxon:10090"
/clone="UUGC2M0274N14"
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                      /note="Vector: U3NeoSV1"
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Location/Qualifiers
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Fax: 801 585 7177
                                                                                                                                                                        Query Match
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AZ990555/c
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(http://www.jax.org/resources/documents/dhares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwap42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and
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purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R., Tingey,A., von Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
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/lab host="B. Coli strain XL10-Gold, T1-resistant, F-"
/lab host="B. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse lobb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
Laboratory Mouse DNA Resource
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                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                             Query Match
47.3%; Score 10.4; DB 8; Length 22;
Best Local Similarity 91.7%; Pred. No. 2.3e+06;
Matches 11; Conservative 0; Mismatches 1; Indels
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Ext Error: 0.00
Plate: 0519 row: A column: 09
Seg primer: CGTTCTAAAACGACGCCAGT
Class: plasmid ends
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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/strain="C57BL/6J"
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Location/Qualifiers
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Mus musculus
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I (bases 1 to 19)
S Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M., Underwood, K., Steptoc,M., Theising,B., Allen,M., Bowers,Y., Underwood,K., Steptoc,M., Theising,B., Allen,M., Bowers,Y., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Washu Zebrafish EST Project 1998
L Unpublished (1998)
Contact: Stephen L. Johnson
Washington University School of Medicine
Washington University School of Medicine
Fax: 14 286 1810
purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XIIO-Gold (Stratagene) cells and selected for ampicillin resistance."
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ED70407.y1 Zebrafish WashU MPIMG EST Danio rerio cDNA clone
IMAGE:3717229 5' similar to TR:023327 023327 HYPOTHETICAL 108.0 KD
AIS45076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: zbrafish@watson.wustl.edu
CDNA Library Arrayed by:
Matthew Clark. CDNA Library Arrayed by:
Matthew Clark. DNA Sequencing by: Washington University Genome
Sequencing Center Clone distribution: Genome Systems, St. Louis,
Missouri (web address: www.genomesystems.com) (email contact:
Misouri (web address: www.genomesystems.com) (anail contact:
(web address: www.resgen.com) (mail contact: info@eresgen.com) and
RessourcenZentrumPrimarDatenbank, Berlin, Germany (web address:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="26 somite embryos, adult livers, shield
stage embryos"
/lab host="XL1-blue MRF"
                                                                                                                                                                                                           Gaps
                                                                                                                                                      46.4%; Score 10.2; DB 8; Length 21; 80.0%; Pred. No. 2.9e+06; ive 0; Mismatches 3; Indels
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Possible reversed clone: similarity on wrong strand
Seg primer: T3 ET from Amersham
High quality sequence stop: 1
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'db xref="taxon:7955"
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Danio rerio
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                                                                                                                                                                                                                                                             6 TTACAGGTAGAAAG 20
                                                                                                                                                                                                                                                                                                       16 Trgcaggrarraag 2
                                                                                                                                                                                                           12; Conservative
                                                                                                                                                        Query Match
Best Local Similarity
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AI545076
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JOURNAL
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by Matthew Clark (Lehrach lab; ICRF, London and Max Planck Institut fuer Molekulare Genetik, Berlin). CDNAs for EST analysis were selected following oligonucleotide hybridization fingerprinting of arrayed clones from zebrafish late somitogenesis (26 ss), adult liver or embryonic shield stage (5.6 h) libraries. Fingerprint data were used to computationally cluster cDNAs, and a single cDNA from each cluster was chosen for sequencing. In some cases multiple members of the same cluster were sequenced to assess clustering parameters or single clones were sequenced additional times to assess quality
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                            45.5%; Score 10; DB 1; Length 19; 72.2%; Pred. No. 3.6e+06;
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Insert Length: 10000 Std Error: (
Plate: 0007 row: F column: 04
Seg primer: CACACAGGAAACAGCTATGACC
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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
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University of Utah Genome Center
University of Utah
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/clone="UUGC2M0007F04"
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Location/Qualifiers
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Fax: 801 585 7177
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Best Local Similarity
Matches 13; Conserv
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AZ775273/c
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.
E (bases I to 20)
E 1 (bases I to 20)
E 2 (bases I to 20)
E 2 (bases I to 20)
E 3 (bases I to 20)
E 4 (bases I to 20)
E 5 (bases I to 20)
E 6 (bases I to 20)
E 7 (bases I to 20)
E 8 (bases I to 20)
E 9 (bases I to
                                             AZ585902
1M0391M24F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
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72.2%; Pred. No. 3.6e+06;
tive 0; Mismatches 5; Indels
                                                                                                           clone UUGC1M0391M24 F, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0391 row: M column: 24
Seq primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Mus musculus"
/mol_type="genomic DNA"
fatrain="C57BL/6J"
/db xref="taxon:10090"
/clone="UUGC1M0391M24"
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Mus musculus
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Best Local Similarity 72.2
Matches 13; Conservative
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Fax: 801 585 7177
Email: ddunn@genet
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84112, US
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RESULT 13
AZ585902
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                        polynuclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pw042 (gill491/81141gb|AR129072.1), a copy number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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/note="Vector: Ml3mp19; The cDNA library of
Schizosaccharomyces pombe was prepared by cloning cDNA
schizosaccharomyces pombe was prepared by cloning cDNA
sequences was not always from 5' to 3'. The cDNA data of
Schizosaccharomyces pombe are available for searching on
the World Wide Web. (URL, http://www.nirs.go.jp)"
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Morimyo,M. and Mita,K.
Identification of expressed sequence tags of Schizosaccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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was blunt end-repaired with T4 DNA polymerase and T4
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Contact: Mitsuoki Morimyo
Contact: Mitsuoki Morimyo
Genome Research Group
National Institute of Radiological Sciences
National Institute of Radiological Sciences
P-1, Anagawa-4-chome, Inage-ku, Chiba, Chiba 263-8555, Japan
Email: morimyo@nirs.go.jp.
Location/Qualifiers
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mol_type="mRNA"
strain="972"
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Schizosaccharomyces pombe
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/clone="spc02889"
/sex="h_minus"
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Best Local Similarity 72.2°
Matches 13; Conservative
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(http://www.jax.org/resources/documents/dhares/). The DNA was hydrodynamically sheared by repeated passage through a was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwdAq1432114[gb]AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                            AZ828233 21 bp DNA linear GSS 20-FEB-2001
2M0105B09F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGC2M0105B09 F, genomic survey sequence.
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
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/clone lib="Mouse lokb plasmid UUGCIM library"
/note=""vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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strain="C57BL/6J"
/db xref="taxon:10090"
/clone="UUGC2M0105B09"
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Insert Length: 10000 Std Error:
Plate: 0105 row: B column: 09
Seg primer: CGTYGTAAACGACGGCCAGT
Class: plasmid ends
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University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Rese
84112, USA
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Location/Qualifiers
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Mus musculus
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Matches 10; Conservative
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Fax: 801 585 7177
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Bukaryotta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

I (bases 1 to 21)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weiss, R.,

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah

Rm. 300, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA
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2M0105B09F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC2M0105B09 F, genomic survey sequence.
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/clone_lib="Mouse lokb plasmid UTGCIM library"
/note="Wector: PWD4ZLY; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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45.5%; Score 10; DB 8; Length 21;
Best Local Similarity 72.2%; Pred. No. 3.6e+06;
Matches 13; Conservative 0; Mismatches 5; Indels
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Ext Error: 0.00
Plate: 0.105 row: B column: 09
Seg primer: CGTTCTAAAACGACGGCCAGT
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/mol_type="genomic DNA"
/strain="C57BL/6J"
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'clone="UUGC2M0105B09"
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Fukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.

E 1 (bases 1 to 19)
S Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.,
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
University of Utah
                                                                                                                                                                                                                                                                                                                                 //db xref="taxon:39947"
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/tibabue_type="callus"
/tibabue_type="callus"
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/lab_host="B_coli DH10B"
/lab_host="B_coli DH10B"
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/lab_host="Coli
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Genomics and Genetics Institute, GreenGene Biotech Inc., Division of Bioscience and Bioinformatics, MyongJi University
Yongin, KyeongGi, Korea
13 1330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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                                                                                                                                                                                                                                                    /organism="Oryza sativa (japonica cultivar-group)"
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Insert Length: 10000 Std Error: 0.00
Plate: 0132 row: I column: 03
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Seg primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers
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/cultivar="Nackdong"
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Fax: 801 585 7177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  UNNOCSVI gene frap. Tag generated by plasmid rescue. Additional sequence information and target gene cloning can be generated. ES cell line harboring insertion mutation of target gene is available. Sequence analysis available from http://l40.193.242.7/esdb/public_search_frame.php?PST=PST5288-NL.Se
                                         13 bp DNA linear GSS 18-MAR-2004
PST$288-NL.Seq MICB1 Mus musculus genomic clone PST$288-NL.Seq,
genomic survey sequence.
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Oryza sativa (japonica cultivar-group)
Coryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
I (basea; I to 19)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Unpublished (2003)
Contact: Nahm B.H.
                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
1 (bases 1 to 13)
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Manitoba Institute of Cell Biology, Universitry of Manitoba
ON5029, 675 McDermot Ave, Winnipeg, MB R3E 0V9, Canada
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /cell_type="Embryonic stem cell"
/cell_line="Dalh (J1 subclone)"
/clone_lib="MICB1"
/note="Vector: U3NeoSV1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44.5%; Score 9.8; DB 9;
84.6%; Pred. No. 4.2e+06;
tive 0; Mismatches 2;
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/strain="129 sv"
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/clone="PST5288-NL.Seq"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: hicksgg@cc.umanitoba.ca
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                                                                                                                                                                                                                                                           Mus musculus (house mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 CATGTTACAGGTA 14
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Unpublished (2002)
Contact: Hicks GG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11; Conservative
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Fax: 204 787 2190
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Class: Gene Trap.
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AUTHORS
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Gaps

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Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Bunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weise, R.
                                             /lab_host="E. Coli strain XLIO-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/60 (male) was obtained from the Jackson
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44.5%; Score 9.8; DB 8; Length 19
Best Local Similarity 84.6%; Pred. No. 4.5e+06;
Matches 11; Conservative 0; Mismatches 2; Indels
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Insert Length: 10000 Std Error: 0.00
Plate: 0464 row: C column: 20
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Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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/clone="UUGC2M0071P14"
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Location/Qualifiers
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Mus musculus
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Fax: 801 585 7177
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                                                                                                                                                                           (http://www.jax.org/resources/documents/dhares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwalp4 (gql 4732114[gb]AF129772.1), a copy.number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. ooli Xilio-Gold (Stratagene) cells and selected for ampicillin resistance."
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Winiversity of Utah
84112, USA
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                           /clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42Iv; Purified genomic DNA from M.
musculus C57BL/GJ (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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Dunn, D., Agogar, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
                                                        lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
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Insert Length: 10000 Std Brror: 0.00
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Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
     clone="UUGC1M0132103"
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Fax: 801 585 7177
Email: ddunn@genet
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Best Local Similarity
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Lifett Submission Balzergue S., UMRGV, INRA/CNRS, 2 rue gaston Cremieux, 91057 Evry cedex, FRANCE
Gaston Cremieux, 91057 Evry cedex, FRANCE
PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versaillee). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at thtp://dbsgap.versailles.inra.fr/publiclines/. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).
                                                                                                                                                                                                 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gal electrophoresis. Vector DNA was prepared from a derivative of pMAP2 (gql 4732114 [gb] AP129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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T-DNA integration into the Arabidopsis genome depends on sequences
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                                             /lab host="B. Coli strain XLIO-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD4ZIY; Purified genomic DNA from M.
musculus C57BL/63 (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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GSS; left border; T-DNA flanking sequence.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
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EMBO Rep. 3 (12), 1152-1157 (2002)
22363535
'clone="UUGC2M0056K07"
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Best Local Similarity 84.69
Matches 11; Conservative
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Balzergue, S.
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                                                 /Bab. maile" Loli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/clone_lib="Wouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources/documents/dnares/). The DNA
was blut cand-repaired by repeated passage.through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically sheared by repeated passage.through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerses and T4
polymuclectide kinase. Adaptor oligonuclectides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarces gel
electrophoresis. Vector DNA was prepared from a derivative
of pwD42 (gi|4732114|gp|AR129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli Xii0-Gold (Stratagene) cells
and selected for ampicillin resistance."
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Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, M., Stokes, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)

Contact: Robert B. Weiss
University of Utah Genome Center
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Insert Length: 10000 Std Error: 0.00
Plate: 0056 row: K column: 07
Seq primer: CGTGTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
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/strain="C57BL/6J"
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   clone="UUGC1M0464C20"
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Fax: 801 585 7177
Email: ddunn@qenet
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Query Match
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Fax: 801 585 7177
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E. (bases 1 to 21)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Really, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von Diamid inserts

L. Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
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1M0215E12R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
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                                                                                                                                     /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
                                                                                                                                                                                                                                                                                                                                Gaps
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1. .20
/organiem="Arabidopsis thaliana"
/mol type="genomic DNA"
culfivar="Wassillewskija"
/db xref="taxon:3702"
/clone="435803"

    20 / note="T-DNA flanking sequence left border"

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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0215 row: E column: 12
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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/mol_type="genomic DNA"
/strain="C57BL/6J"
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clone="UUGCIM0215E12"
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Location/Qualifiers
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Mus musculus
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84.6%;
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Best Local Similarity 84.6'
Esches 11; Conservative
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adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWH22 (gi|4732114|gb|AP129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into adaptored beneficially-competent B. coli X110-Gold (Stratagene) cells and selected for ampicillin resistance."
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AZ48J078 105-OCT-200 100308H04R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0308H04 R, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                           Score 9.8; DB 8; Length 21;
Pred. No. 4.5e+06;
); Mismatches 2; Indels
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Insert Length: 10000 Std Error: 0.00
Plate: 0308 row: H column: 04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
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Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends

    .21
    /organism="Mus musculus"

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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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/clone="UUGC1M0308H04"
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Location/Qualifiers
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Mus musculus
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us-09-743-825-7.max.rst

ORIGIN

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10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwb42 (gil4732114 fgl AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored wector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance.
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adaptored DNA was purified and size-selected for a 9.5 to
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/clone lib="Mixed stage fosmid library of P. pacificus
var. California"
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Srinivasan, J., Otto, G.W., Kahlow, U., Geisler, R. and Sommer, R.J.
AppaDB: an AcedB database for the nematode satellite organism
Pristinonchus pacificus
Nucleic Acids Res. 32 (1), D421-D422 (2004)
Contact: Sommer RJ
                                                                                                                                                                                                                                                                                                                                                                Gaps
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Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
Seg primer: T7
Class: fosmid ends.
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Neodiplogasteridae; Pristionchus.
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                                                                                                                                                                                                                                                                                                          Score 9.8; DB 8; Length 22;
Pred. No. 4.6e+06;
); Mismatches 2; Indels
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Coganism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
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Pristionchus pacificus
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Best Local Similarity 84.6
Matches 11, Conservative
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AZ396022
LOCUS
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TITLE
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COMMENT
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                          10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD4 (gi|4732114 |gb|AF129072.11), a copy-numble inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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     adaptored DNA was purified and size-selected for a 9.5 to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AZ786362
2M0031N16R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0031N16 R, genomic survey sequence.
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/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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84112, USA
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Pred. No. 4.5e+06;
); Mismatches 2; Indels
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Pax: 801 585 7177

Email: ddunm@genetics.utah.edu
Insert Length: 10000 Std Brror: 0.00
Plate: 0031 row: N column: 16
Seq primer: CACACAGGAAACAGCTAATGACC
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/strain="C57BL/63"
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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clone="UUGC2M0031N16"
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Location/Qualifiers
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Best Local Similarity 84.6%;
Matches 11; Conservative
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DEFINITION

ORGANISM

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TITLE

VERSION KEYWORDS SOURCE ACCESSION

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muscular C7/bay, Marse DAR Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xili0-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 20) Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longarce, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhauseern, A. and Wright, D., Weiss, R., Tingey, A., von plasmid inserts
2M0033016F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC2M0033016 F, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /lab_host="B. Coli strain XL10-Gold, Tl-resistant, F-"
/clone lib="Mouse lokb plasmid UGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from musculus C57BL/6J (male) was obtained from the Jackson
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0033 row: O column: 16
Seg primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0033016"
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High quality sequence stop: 20.
Location/Qualifiers
                                                                                                                                                    Mus musculus (house mouse)
                                                                                   AZ787298.1 GI:12925926
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                         Mus musculus
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Best Local S
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CL687844/c
LOCUS
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      DEFINITION
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KEYWORDS
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                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Manmalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 2E 1 (bases 1 to 20)

SS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahamoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

U pupullished (2000)

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch oritice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymuclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gal electrophoresis. Vector DNA was prepared from a derivative of pwalp42 (gil 4732114|gp|AR129072.1), a copy.number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to
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   1M0160J20F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunmgenetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0160 row: J column: 20
Seq primer: CGTTGTAAAACGACGGCCAGT
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/strain="C57BL/6J"
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High quality sequence stop: 20.
Location/Qualifiers
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                                                                                                                                                          Mus musculus (house mouse)
                                                                                               AZ396022.1 GI:10511094
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Best Local Similarity 75.0
Matches 12; Conservative
                                                                                                                                                                                         Mus musculus
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Gaps .; 0 GSS 09-JUL-2004

RESULT 28 AZ787298 LOCUS

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ORIGIN

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end was generated during the R&D process and may have higher chance
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/organism="Mus musculus"
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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/strain="C57BL/6J"
                                                                                                                                                                                                                  /mol_type="genomic_DNA"
/db_xref="taxon:9598"
/clone="RP43-078H02.T7"
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/clone="UUGC1M0029P03"
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                                                                                                  : pBACe3.6
: EcoRI
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                    of clone tracking errors
PRIMERS
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Best Local Similarity 75.0%
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Fax: 801 585 7177
                                                                  Sequencing:
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R.Site 2
                                                                                                      Vector
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AZ312945/c
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Clones are derived from the chimpanzee BAC library RP-43 This BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AG197947 21 bp DNA linear GSS 06-MAR-2004
Pan troglodytes DNA, clone: RP43-078H02.T7, genomic survey
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        PRIO147d G03 2 - PRIO147d.BR (20) Mixed stage fosmid library of P. pacificus var. California Pristionchus pacificus genomic, genomic
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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/clone lib="Mixed stage fosmid library of P. pacificus
var. California"
/note="Vector: pEpifos-5 Fosmid vector"
                                                                                                                                                              Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida; Neodiplogasteridae; Pristionchus.

1 (Jases 1 to 20)
Srinivasas 1, Otto, G.W., Kahlow, U., Geisler, R. and Sommer, R.J. AppaDB: an AcedB database for the nematode satellite organism Pristionchus pacíficus
Nucleic Acids Res. 32 (1), D421-D422 (2004)
Contact: Sommer RJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C.J.,
Park, H., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C.J., Hoon, S.T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H. BAC end sequences of Library RP-43
                                                                                                                                                                                                                                                                                                                                                                                          Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
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Max-Planck-Institute for Developmental Biology
Mapmannetr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371

    .20
    .coganism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"

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75.0%; Pred. No. 5.6e+06;
tive 0; Mismatches 4;
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                                                                                                                            Pristionchus pacificus
Pristionchus pacificus
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Class: fosmid ends.
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                                                survey sequence.
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AG197947/c
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Criurognathi; Muridae; Murinae; Mus.
1 (Dases 1 to 19)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weise, R.
Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A2312945
IM0029P03F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
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84112, USA
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                                                                                                                                                                                                                                                                                                                        Gapa
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                                                                                                              /sex="male"
/cell_type="lymphocytes"
/clone_lib="RP-43 Chimpanzee Male BAC Library"
                                                                                                                                                                                                                                                     Score 9.6; DB 9; Length 21; Pred. No. 5.7e+06; 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0029 row: P column: 03
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence Stop: 19.
/organism="Pan troglodytes"
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(http://www.inace.una.ces/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymuclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMAP2 (gil #472114|gbl #712104]c) a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli Xillo-Gold (Stratagene) cells and selected for ampicillin resistance."
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Zachgo, S., Stueber, K., Saedler, H., Sommer, H. and Schwarz-Sommer, Z.
Antirrhinum EST collection
Unpublished (2003)
Contact: Schwarz-Sommer Z
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/tissue type="whole plant"
/clone lib="Antirthinum majus whole plant"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42.7%; Score 9.4; DB 8; Length 19; 68.4%; Pred. No. 7e+06; ive 0; Mismatches 6; Indels
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MPI fuer Zuechtungsforschung
Carl-von-Linne Weg 10, D-50829, Germany.
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:4151"
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Antirrhinum majus
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Best Local Similarity 68.4'
Matches 13; Conservative
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AJ796099
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              (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gal electrophoresis. Vector DNA was prepared from a derivative of pubA2 (gql 4732114)[gbl A722072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xiii0-Gold (Stratagene) cells and selected for ampicillin resistance."
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Winsersity of Utah
Winsersity of Utah
84112, USA
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Dun, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Nese, M., Rose, M
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Insert Length: 10000 Std Error: 0.00
Plate: 0004 row: P column: 01
Seg primer: CGTTGTAAACGACGGCCAGT
Laboratory Mouse DNA Resource
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/strain="C57BL/6J"
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/clone="UUGC2M0004P01"
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High quality sequence stop: 19.
Location/Qualifiers
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Mus musculus
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Fax: 801 585 7177
Email: ddunn@qenet
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ACCESSION VERSION KEYWORDS

ORGANISM

REFERENCE AUTHORS

JOURNAL

COMMENT

TITLE

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/lab hose="E" coli strain XL10-Gold, T1-resistant, F-"
/lab hose="E" coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Meouse 10kb plasmid UUGC2M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resources
/nttp://www.jax.org/resources/documents/dnares/). The DNA
was bydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligomucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarces get
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gp|AR129072.1); a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli Xil0-Gold (Stratagene) cells
and selected for ampicillin resistance."
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                                                                                                                                                                    Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 22)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
Dusamid inserts
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
84112, USA
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clone UUGC2M0203K13 F, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Brror: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plate: 0203 row: K column: 13
Seg primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
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University of Utah Genome Center
University of Utah
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/strain="C57BL/6J"
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/clone="UUGC2M0203K13"
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                                                                                                                 Mus musculus (house mouse)
                                                          AZ942905.1 GI:13806556
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Best Local Similarity
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TA82F07Q/c
LOCUS
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                                                                                                                       SOURCE
                             ACCESSION
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                                                                                                                                              Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bummalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Lo 21)
I (bases 1 to 21)
S Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
University of Utah Genome Center
University of Utah Genome Center
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
Fel: 801 585 5606
Fax: 801 585 7177
Email: ddunnégenetics.utah.edu
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LOCUS AZ942905 26-APR-2001
DEFINITION 2M0203K13F Mouse 10kb plasmid UUGC2M library Mus musculus genomic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S. 2030 E., SLC, UT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"/clone lib="Mouse 10kb plasmid UGCIM library."
/note="Vector: PWD42ry; Purified genomic DNA from M.musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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   clone UUGC1M0212P03 R, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bmail: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seq primer: CACACAGGAAACAGCTATGACCClass: plasmid ends
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|mol_type="genomic DNA"
|strain="C57BL/6J"
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Location/Qualifiers
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/clone="UUGC1M0212P03"
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                                                                                                                          Mus musculus (house mouse)
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AZ428984.1 GI:10552913
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AZ612157.1 GI:11734347
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Matches 11; Conservative
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Fax: 801 585 7177
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Hall, N., Bowman, S., Lennard, N. J., Doggett, J., Atkin, R.,
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Melville, S.E., Rajandream, M.A. and Barrell, B.G.
Direct Submission

Lineat Submission

Nobject, Sanger Centre, The Wellcome Trust Genome Gampus, Hinxton,
Cambridge CB10 ISA, E-mail: barrell@sanger.ac.uk and
nhl@sanger.ac.uk

Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTAt 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: nelsayed@tigr.org
Details of T. brucel sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
Location/Qualifiers
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Amphibia; Batrachia; Caudata; Salamandroidea; Ambystomatidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                       Sukaryota, Euglenozoa, Kinetoplastida; Trypanosomatidae,
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Tel: 0049 351 210 2620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
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/clone="82f07"
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Contact: Elly M. Tanaka
       survey sequence
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CO780477.1 GI:50996457
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1 (bases 1 to 19)
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                                                                                                                  Irypanosoma brucei
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AZ612157 11082 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0438L21 R, genomic survey sequence.
                                                                                                                                                                          /tissue type="real Blastema" | /tissue type="real type="regenerating tail blastema" | /coll type="regenerating tail blastema" | /colne_lib="do-Day Axolot! Tail Blastema (6DAxBL) | /colne_lib="do-Day Axolot! Tail Blastema (6DAxBL) | /note="vector: pcMVSport6; Site_l: Not1; Site_2: Sall; Unnormalized cDNA plasmid library prepared by Invitrogen. Size fractionated mRNA was polydT primed and cloned into Not!-Sall site of pcMVSport6. Bacterial host is EMDH10B-TONA. Average insert size is 1.67 kB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
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0
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78.6%; Pred. No. 8.7e+06;
tive 0; Mismatches 3; Indels
                                             ď.
Email: tanaka@mpi-cbg.de
Plate: BlObpb row. 65 column: A
Seq primer: GCA CAT TAG GCC TAT TTA GGT GAC
Location/Qualifiers
                                                                                                             /organism="Ambystoma mexicanum'
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Class: plasmid ends
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/strain="C57BL/6J"
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/clone="UUGC1M0438L21"
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Location/Qualifiers
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Insert Length: 10000 Std Err
                                                                                                                                  /mol_type="mRNA"
/db_xref="taxon:8296"
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musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was bydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWM22 (gi|4732114|gb|AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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/clone lib="Schizosaccharomyces pombe late log phase cDNA"
/clone lib="Schizosaccharomyces pombe was prepared by cloning cDNA
schizosaccharomyces pombe was prepared by cloning cDNA
into the Smal site of Milmp19 DNA and the direction of DNA
sequences was not always from 5' to 3'. The cDNA data of
Schizosaccharomyces pombe are available for searching on
the World Wide Web. (URL, http://www.nirs.go.jp)"
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Identification of expressed sequence tags of Schizosaccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AU008312 Schizosaccharomyces pombe late log phase CDNA Schizosaccharomyces pombe late log phase CDNA Schizosaccharomyces pombe CDNA clone spc03191, mRNA sequence.
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Genome Research Group
National Institute of Radiological Sciences
National Institute of Radiological Sciences
9-1, Anagawa-4-chome, Inage-ku, Chiba, Chiba 263-8555, Japan
Email: morimyo@nirs.go.jp.
Location/Qualifiers
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Schizosaccharomyces pombe
Bukaryota, Fungi, Ascomycota, Schizosaccharomycetes,
Schizosaccharomycetales, Schizosaccharomycetaces,
Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41.8%; Score 9.2; DB 8; Length 19; 78.6%; Pred. No. 8.7e+06; Live 0; Mismatches 3; Indels
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Best Local Similarity 73.3%; Pred. No. 8.9e+06;
Matches 11; Conservative 0; Mismatches 4; Indels
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AU008312.1 GI:3344770
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                                                                (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymuclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwalp42 (gel #4722114)[gh]AF12977.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xii0-Gold (Stratagene) cells and selected for ampicillin resistance."
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Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.
E 1 (bases 1 to 19)
S 1 (bases 1 to 19)
S 1 (bases 1 to 10)
S 1 (bases 1 to 19)
S 2 (bun, D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacze,S., Mahmoud,M., Meenen,E., Pedersen,T., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
University of Utah Genome Center
University of Utah Genome Center
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                musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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/note="Vector: PWD42nv; Purified genomic DNA from M.
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Pax: 801 585 7177

Email: ddunm@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0086 row: P column: 05
Seq primer: CACACAGGAAAACAGCTAATGACC
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/mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="UUGC2M0086P05"
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High quality sequence stop: 19.
Location/Qualifiers
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Search completed: August 12, 2005, 09:54:57 Job time : 1787 secs

AR402107 Sequence AX217836 Sequence BD067607 Enzymatic AR160744 Sequence AR310829 Sequence BD238283 Accelerat AX804694 Sequence L77539 Canis famil CQ786885 Sequence L24208 Dog (Clone: BD138203 Antienne:	CO794181 Sequence CQ800150 Sequence CQ800150 Sequence AR230770 Sequence AR312230 Sequence AR312230 Sequence AR355425 Sequence AR355425 Sequence AX167860 Sequence AX16786 Sequence AX086738 Sequence AX086738 Sequence AX086738 Sequence AX086736 Sequence AX086736 Sequence AX086736 Sequence	AR402110 Sequence AX578318 Sequence AX578319 Sequence AX690586 Sequence AX690586 Sequence BD067610 Brzymatic AR293947 Sequence AR292924 Sequence AX129249 Sequence AX129249 Sequence AX129249 Sequence AX129249 Sequence AX1295618 Sequence AX571920 Sequence AX571920 Sequence AX129618 Sequence AX129618 Sequence AX129618 Sequence AX130183 Sequence	BD184497 Method an CQ959917 Sequence AX396902 Sequence AX742644 Sequence L77371 Canis famil BD241765 Embryonic AX296909 Sequence AX293910 Sequence AX250343 Sequence AX250343 Sequence AX167790 Sequence AX167790 Sequence AX167790 Sequence AX16790 Sequence AX16799 Sequence AX137951 Sequence AX137951 Sequence AX137951 Sequence AX137969 Sequence AX137969 Sequence AX31283 Sequence AX312841 Sequence
11.8 56.2 17 11.8 56.2 17 11.8 56.2 20 11.8 56.2 20 11.8 56.2 20 11.8 56.2 20 11.8 56.2 21 11.6 55.2 21 11.6 55.2 21	11.6 55.2 20 11.6 55.2 20 11.7 4 54.3 20 11.8 54.3 20	111.2 53.3 11.2 11.2 53.3	11.2 53.3 11.2 52.4 11.3 52.4 11.5 52.4 12.5 52.4 13.5 52.4 13.5 52.4 13.5 52.4 13.5 52.4 14.5 52.4 15.5 52.4
0000 00000			0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd. nucleic search, using sw model August 12, 2005, 09:25:17; Search time 1566 Seconds (without alignments) 649.783 Million cell updates/sec	US-09-743-825-8 1 ctggcgtatctgaagagtctg 21 1 ctggcgtatctgaagagtctg 21 1 ctggcgtatctgaagagtctg 21 1 indexity Nuc Gapop 10.0, Gapext 1.0 4708233 seqs, 24227607955 residues of hits satisfying chosen parameters: 892778 of length: 0 q length: 0 q length: 21 ng: Minimum Match 0% Maximum Match 100% Listing first 100 summaries		No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, derived by analysis of the total score distribution. SUMMARIES
OM nucleic - r Run on:	Title: Perfect score: Sequence: Scoring table: Searched: Total number of Minimum DB seq Maximum DB seq Post-processing	Database :	Result No. Score grand is day Result No. 3 12.8 C 3 12.8 C 4 12.8 C 5 12.8 C 6 12.2 C 7 12.2 C 9 12.2 C 10 12.2 C 11 12.2 C 11 12.2 C 12 11.8 I 11 12.2 C 13 11.8 I 11 12.2 C 14 11.8 I 16 11.8 I 17 11.8 I 18 11.8 I 18 11.8 I 19 11.8

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unidentified
unidentified
unclassified.

unclassified.

1 (bases 1 to 17)

RAKHAT,S., Fell,P. and Mcswiggen,J.A.

Enzymatic nucleic acid treatment of diseases or conditions related to levels of epidermal growth factor receptors

RIBOZYWE PHARMACEUTICALS INC,ASTON UNIV

OS Unidentified

NN JP 2001511003-A/448

PD 07-AUG-2001

PF 14-JAN-1999 UP 1998532913

PR 31-JAN-1997 US 60/036476,04-DEC-1997 US 08/985162 PI
SAGHIR AKHTAR, PATRICIA FELL, JAMES A MCSWIGGEN PC
C12N9/00, C07K14/71

CC Strandedness: Single;
CC Topology: Linear;
CC Enzymatic nucleic acid treatment of diseases or conditions CC
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Enzymatic nucleic acid treatment of diseases or conditions related to levels of epidermal growth factor receptors.

BD067608
BD67608.1 G1:22613211
UP 2001511003-A/448.
               PAT 18-DEC-2003
                                                                                                                                    1. (bases 1 to 17)
Akhtar,S., Fell,P. and McSwiggen,J.A.
Brymatic nucleic acid treatment of diseases of conditions related
to levels of epidermal growth factor receptors
Patent: US 6623962-A 448 23-SEP-2003;
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                 linear
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Location/Qualifiers
         Sequence 448 from patent US 6623962. AR402108

    .17
    /organism="unidentified"
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/db_xref="taxon:32644"

                                                                                                                                                                                                                                             /organism="unknown"
/mol_type="genomic DNA"
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16 GTATCGAAAGAGTCTG 1
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BD255497 Regulatio
AR186193 Sequence
AX322224 Sequence
AX217098 Sequence
AX217097 Sequence
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Buell,G.N., Surprenant,A. and Kawashima,E.
Methods of screening modulators of mammalian P2X7 purinergic
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Buell, G.Nutter., Surprenant, A. and Kawashima, E. Purinergic receptor
Patent: US 6133434-A 3 17-OCT-2000;
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/organism="unknown"
/wol_type="unassigned DNA"
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Location/Qualifiers
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Sequence 3 from patent US 6133434.
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Sequence 3 from patent US 6509163.
AR275648
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BD255495
BD255496
BD255497
AR186193
AR322824
AX217098
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/organism="unknown"
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Best Local Similarity 100.
Matches 13; Conservative
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RESULT 5 A17234/c LOCUS DEFINITION

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BD067609 17 bp RNA linear PAT 27-AUG-2002 Enzymatic nucleic acid treatment of diseases or conditions related to levels of epidermal growth factor receptors.
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1 (bases 1 to 17)

Akhtar, S., Fell, P. and Mcswiggen, J.A.

Enzymatic nucleic acid treatment of diseases or conditions related to levels of epidermal growth factor receptors

Patent: JP 2001511003-A 449 07-AUG-2001;

RIBOZYME PHARMACEUTICALS INC, ASTON UNIV

OS Unidentified

PN JP 2001511003-A/449
                1 (bases 1 to 17)
Akhtar,S., Fell,P. and McSwiggen,J.A.
Enzymatic nucleic acid treatment of diseases of conditions related to levels of epideral growth factor receptors
Patent: US 6623962-A 449 23-SEP-2003;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shannon,M., Gu,Y. and Nguyen,C.T.
Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
mdz12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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tive 0; Mismatches 3; Indels
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82.4%; Pred. No. 3.3e+05;
tive 0; Mismatches 3;
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Sequence 3317 from Patent EP1281758.
AX690585
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/db_xref="taxon:9606"
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/organism="unknown"
/mol_type="genomic DNA"
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Location/Qualifiers
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Matches 14; Conservative
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Best Local Similarity 82.4
Matches 14; Conservative
  Unclassified.
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Unclassified.
Unclassified.
1 (base 1 to 20)
Craig, S., Hunter, M. George., Edwards, R. Mark., Czaplewski, L. George.
and Gilbert, R. James.
Stem cell inhibiting proteins
Patent: US 5855301-A 134 05-JAN-1999;
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    .20
    forganism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

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synthetic construct
other sequences; artificial sequences.
1 (bases 1 to 20).
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Patent: WO 9313206-A 134 08-JUL-1993;
Location/Qualifiers
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Sequence 449 from patent US 6623962.
AR402109
AR402109.1 GI:40149559
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16 GTATCGAAAGAGTCTG
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Telerman, A., Amson, R. and Tuijnder, M.
Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or resistance to viruses and the use thereof as medicaments
Patent: WO 0325577-A 3472 27-MAR-2003;
Molecular Engines Laboratories (FR)
Location/Qualifiers
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Antisense modulation of il-1 receptor-associated kinase-1
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                                                                           Score 12.2; DB 6;
Pred. No. 3.3e+05;
0; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1. 20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
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                                                                                                                                                                                                                                                              DNA
                                                                                                                                                                                                                                                                                                                                                                           other sequences; artificial sequences.
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Patent: WO 03104458-A 79 18-DEC-2003;
ISIS PHARMACEUTICALS, INC. (US)
Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
1. .20
/organism="unknown"
/mol_type="unassigned DNA"
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Sequence 79 from Patent WO03104458.
AX962823
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                                                                           Query Match 58.1%;
Best Local Similarity 82.4%;
Matches 14; Conservative C
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Cesarman B. and Knowles D.M.
DNA encoding proteins of Kaposi's sarcoma associated herpesvirus
Patent: US 6093806-A 8 25-UUL-2000;
Location/Qualifiers
                                                                                                Topology: Linear; Enzymatic nucleic acid treatment of diseases or conditions related to a respect of epidermal growth factor receptors
                                 08/985162 PI
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Cesarman, E., Arvanitakis, L., Knowles, D.M. and Mesri, E. KSHV positive cell lines
Patent: US 5908773-A 8 01-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ch 58.1%; Score 12.2; DB 6; Length 20; l. Similarity 82.4%; Pred. No. 3.3e+05; 14; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                            58.1%; Score 12.2; DB 6; Length 17; 82.4%; Pred. No. 3.3e+05; tive 0; Mismatches 3; Indels
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PD 07-AUG-2001
PF 14-JAN-1998 UF 1998512913
PF 14-JAN-1997 US 60/036476,04-DEC-1997 US SAGHIR AKHTAR, PATRICIA FELL, JAMES A MCSWIGGEN PC C12N9/00,C07K14/71
CC Strandedness: Single;
CC Topology: Linear;
CC Enzymatic nucleic acid treatment of diseases
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    .17
    /organism="unidentified"
    /mol_type="genomic RNA"
    /db_xref="taxon:32644"

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/organism="unknown"
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1 (bases 1 to 17)
Racaniello,V., Tatem,J.Marie. and Weeks-Levy,C.L.
Method for producing RNA viruses from cDNA
Patent: US 6136570-A 4 24-OCT-2000;
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                                     Unknown.
Unclassified.
I (basse I to 17)
Racaniello, V., Tatem, J. Marie. and Weeks-Levy, C.L.
Method for producing RNA viruses from CDNA
Patent: US 5834302-A 4 10-NOV-1998;
Location/Qualifiers
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1 (bases 1 to 17)
Racaniello,V., Tatem,J.M. and Weeks-Levy,C.L.
Method for producing RNA viruses from CDNA
Patent: US 5525715-A 4 11-JUN-1996;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             56.2%; Score 11.8; DB 6;
llarity 86.7%; Pred. No. 5.5e+05;
Conservative 0; Mismatches 2;
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/organism="unknown"
/mol_type="unassigned DNA"
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/wol_type="unassigned DNA"
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/mol_type="unassigned DNA"
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Sequence 4 from patent US 6136570.
AR135992. GI:14476664
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Sequence 4 from patent US 5525715.
122067.
122067.1 GI:1602421
 AR053990.1 GI:5978852
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Unknown.
Unclassified.
1 (bases 1 to 17)
1 hompson, J.D. and Draper, K.G.
Thompson, J.D. and Draper, K.G.
The bcl-2 gene
Of the bcl-2 gene
Patent: US 5750390-A 18 12-MAY-1998;
Location/Qualifiers
                                                                                                                                                                                                                                   Unknown.
Unknown.
Unknown.
Unclassified.
1 (bases 1 to 16)
1 vocy.p., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
Patent: US 6566127-A 5737 20-MAY-2003;
Location/Qualifiers
                 Gaps
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Pred. No. 4.2e+05;
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Sequence 18 from patent US 5750390.
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Sequence 4 from patent US 5834302.
AR053990
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AR007304.1 GI:3966788
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Best Local Similarity 86.7
Matches 13; Conservative
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Best Local Similarity 86.7
Matches 13; Conservative
 Similarity 100.
                                             7 TATCTGAAGAGT 18
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   Best Local
Matches 1
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RESULT 15 AR007304

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AUTHORS TITLE

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RESULT 14 AR328335

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unclassified.

In [bases 1 to 77]

State Arthrey Services and Mcswiggen, J.A.

Enzymatic nucleic acid treatment of diseases or conditions related to levels of epidermal growth factor receptors

A patent: JP 2001511003-A 447 O7-AUG-2001;

RIBOZYME PHARMACEUTICALS INC, ASTON UNIV
OS Unidentified
PN 07-AUG-2001
PP 14-JAN-1998 JP 1998532913
PR 31-JAN-1997 US 60/036476, 04-DEC-1997 US SAGHIR ARKHRAR, PATRICIA FELL, JAMES A MCSWIGGEN PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BD067607
Enzymatic nucleic acid treatment of diseases or conditions related
to levels of epidermal growth factor receptors.
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Enzymatic nucleic acid treatment of diseases or conditions
related to
                                                                                                             Blatt, L., Mcswiggen, J. and Chowrira, B.M.
Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
Patent: WO 0155103-A 3278 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                              Score 11.8; DB 6; Length 17;
Pred. No. 5.5e+05;
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                                                                                                                                                                                                                                                  /organism="synthetic construct"
/mol type="unassigned RNA"
/mol xref="taxon:32630"
/note="Nucleic Acid"
                                              synthetic construct
synthetic construct
other sequences; artificial sequences.
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AX217836.1 GI:15527897
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86.7%;
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Akhtar, S., Fell, P. and McSwiggen, J.A.
Enzymatic nucleic acid treatment of diseases of conditions related
to levels of epidermal growth factor receptors
Patent: US 6623962-A 447 23-SEP-2003;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                    Tobases 1 to 17)
Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor Patent: US 6566127-A 4438 20-MAY-2003;
Location/Qualifiers
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US 6566127.
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Sequence 447 from patent US 6623962.
AR402107
AR402107.1 GI:40149557
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Sequence 3278 from Patent WO0159103.
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/mol_type="unassigned RNA"
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/mol_type="genomic DNA"
                                                                                                                                                                                                     Sequence 4438 from patent
AR327036
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   56.2%;
86.7%;
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17 TATCGAAGAGTCTG 3
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                                                                 3 GCCGTATCTGAAGAG 17
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optoneous Constructs

(bases 1 to 21)

Barany, F., Liu, J., Kirk, B.W., Zirvi, M., Gerry, N.P. and Paty, P.B.
Accelerated identification of polymorphism of single nucleotide in genome sequencing and alignment of clones
Patent: JP 2002534098-A 118 15-OCT-2002;
CORNELL RESEARCH FOUNDATION INC, SLOAN KETTERING INSTITUTE FOR CANCER RESEARCH
OS Artificial Sequence

PN JP 2002534098-A/118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oreochromis niloticus (Nile tilapia)
Oreochromis niloticus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Actinopterygii, Neopterygii, Teleostei, Buteleostei, Meoteleostei,
Acanthomorpha, Acanthopterygii, Percomorpha, Perciformes,
Labroidei, Cichlidae, Oreochromis.
                                                                                                                                                                                                                                                        PHILIP B PATY
C12N15/09,C12Q1/68,G01N33/53,G01N33/566,G01N37/00,G01N37/00//
                                                                                                                                                    15-OCT-2002
05-JAN-2000 JP 2000592447
06-JAN-1999 US 60/114881
FRANCIS BARANY, JIANZHAO LIU, BRIAN W KIRK, MONIB ZIRVI, NORMAN
GERRY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lie,Y., Slettan,A., Hoeyum,M. and Lingaas,F.
Verification of food origin based on nucleic acid pattern
                                                                                                                                                                                                                                                                                                                  Description of Artificial Sequence: probe/primer FH Location/Qualifiers
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/organism="Oreochromis niloticus
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86.7%; Pred. No. 5.4e+05;
iive 0; Mismatches 2;
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
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Patent: WO 03060160-A 862 24-JUL-2003;
Genomar ASA (NO)
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Sequence 862 from Patent WO03060160.
AX804694
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/db_xref="taxon:8128"
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Matches 13; Conserv
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BD238283
BD238283.1 GI:33048053
UP 2002534098-A/II8.
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1 (bases 1 to 20)
Griffais,R., Hoiseth,S.K., Zagursky,R.J., Metcalf,B.J.,
Sankaran,B. and Fletcher,L.D.
Chlamydia pneumoniae polynucleotides and uses thereof
Patent: US 6559294-A 1366 06-MAY-2003;
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Cowsert, L.M. and Wyatt, J.
Antisense modulation of ARA70 expression
Patent: US 6255110-A 38 03-UUL-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AR310829 20 bp DNA Sequence 1366 from patent US 6559294.
                                                                                                               AR160744 20 bp 1
Sequence 38 from patent US 6255110.
AR160744
                                                                                                                                                                                                                                                                                                                               1. .20
/organism="unknown"
/wol_type="unassigned DNA"

    .20
    /organism="unknown"
    /mol_type="genomic DNA"

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Best Local Similarity 86.7
Matches 13; Conservative
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AR160744/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Original source text: Canis familiaris (library: E. Ostrander, in pBluescript+) adult spleen DNA.
Submitted by: Fred Hutchinson Cancer Research Center Transplantation Biology Dept 1124 Columbia; Mailstop M318
Seattle, WA 98104, USA e-mail: EAOstrander@lbl.gov PCR
Buffer: PCR buffer (Perkin-Elmer/Cetus) PCR Profile:
Denaturation: 94 degrees C for 1.00 minute Annealing: 55 or 59 degrees C for 0.45 minutes POlymerization: 74 degrees C for 5.00 minutes.

Location/Qualifiers
                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi; Mammalia, Butheria, Carnivora, Fissipedia, Canidae, Canis. I (bases I to 20). Ostrander, E.A., Mapa, F.A., Yee, M. and Rine, J. Ostrander, E.A., Mapa, F.A., Yee, M. and Rine, J. One hundred and one new simple sequence repeat-based markers for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  unidentified
unclassified.

1 (bases 1 to 20)
Miraglia, L.J., Nero,P., Graham,M.J., Monia,B.P. and Cowsert,L.M.
Antisense modulation of human MDM2 expression
Patent: JP 2002508944-A 129 26-MAR-2002;
ISIS PHARMACEUTICALS INC
OS Unidentified
PN JP 2002508944-A/129
PD 26-MAR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="genomic DNN"
/db xref="taxon:9615"
/tissue_type="spleen"
/dev stage="adult"
/tissue_lib="E. Ostrander, in pBluescript+"
                                                                                                                       20 bp DNA linear
Dog (Clone: CXX.176) primer for STS 176, 5' end.
L24208
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Antisense modulation of human MDM2 expression.
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llarity 77.8%; Pred. No. 6.9e+05;
Conservative 0; Mismatches 4;
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                                                                                                                                                                                                L24208.1 GI:401855
PCR identification; PCR primer; STS.
1 of 2
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Mamm. Genome 6 (3), 192-195 (1995)
95268214
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JP 2002508944-A/129.
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Canis familiaris
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Best Local Similarity
Matches 14; Conserv
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Location/Qualifiers
                                                          DOGC00505A 21 bp DNA linear STS 10-APR-1996 Canis familiaris STS microsatellite marker (repeat motif in treference clone (GT)9T(TG)4(TA)4(TG)7) DNA, sequence tagged site. L77539
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                                                                                                                                     L77539.1 GI:1261663
STS; PCR identification; microsatellite; sequence tagged site.
Canis familiaris (dog)
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
1 (Dases 1 to 21)
Yuzbasiyan-Gurkan, V., Cao, Y., Gurkan, M., Yuxun, W., Venta, P.J.,
Microsatelite markers for the canine genome
Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                               Original source text: Canis familiaris female adult peripheral
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Method of diagnosing colon and gastric cancers
Patent: WO 2004021010-A 62 11-MAR-2004;
Oncotherapy Science, Inc. (JP); Japan as represented by the president of the university of Tokyo (JP)
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /sex="female"
/cell_type="white blood cells"
/tissue type="peripheral blood"
/dev stage="adult"
1. .21
/note="product size 230"
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Canis familiaris"
/mol_type="genomic DNA"
/db xref="taxon:9615"
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synthetic construct
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Best Local Similarity 86.7
Matches 13; Conservative
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Best Local Similarity 77.8
Matches 14; Conservative
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                    RESULT 27
DOGC00505A/c
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CQ786885/c
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PAT 29-JUL-2004

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/note="The oligonuclectides were prepared by conventional phosphoramidit e synthesis"
            Meijer,C.J. and Snijders,P.J.
Method for detecting and typing of cutaneous hpv and primers and probes for use therein
Patent: WO 2004029302-A 101 08-APR-2004;
Stichting Researchfonds Pathologie (NL)
Location/Qualifiers
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="type-specific detection probe RLBskinHPV 37"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gouliaev, A.H., Holtmann, A., Pedersen, H. and Franch, T. Quasirandom structure and function guided synthesis methods Patent: WO 2004056994-A 29 08-JUL-2004; Nuevolution A/S (DEX) Location/Qualifiers
                                                                                                                                                                                                                          y Match 55.2%; Score 11.6; DB 6; Length 20; Local Similarity 77.8%; Pred. No. 6.9e+05; nes 14; Conservative 0; Mismatches 4; Indels
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Pred. No. 6.9e+05;
0; Mismatches 4;
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
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1 (bases 1 to 20)
Popoff, I and Cowsert, L.M.
Antisense modulation of PARP expression
Patent: US 6451602-A 30 17-SEP-2002;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA
                                                                                                                                                                                                                                                                                                                                                                                                             CQ831775 20 bp DNA Sequence 29 from Patent WO2004056994.
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5 6451602.
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AR230770
                                                                                                                                                                                                                                                                                                                        3 CTGGTATATTGGAAGAGT 20
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Best Local Similarity 77.8%;
Matches 14; Conservative C
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                 26-MAR-1998 US 09/048810
LOREN J MIRAGLIA, PAMELA NERO, MARK J GRAHAM, BRETT P MONIA, LEX
                                                                 COMSERT
CI2N15/09,A61K48/00,A61P9/10,A61P17/06,A61P35/00,C07H21/04//
C12Q1/68,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Meijer,C.J. and Snijders,P.J.
Method for detecting and typing of cutaneous HPV and primers and probes for use therein
Patent: EP 1403384-A 101 31-MAR-2004;
Stichting Researchfonds Pathologie (NL)
Location/Qualifiers
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Antisense modulation of human MDM2 expression FH
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                               ch 55.2%; Score 11.6; DB 6; Length 20;
1 Similarity 77.8%; Pred. No. 6.9e+05;
14; Conservative 0; Mismatches 4; Indels
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                                                                                                                                                                                                               /organism='Unidentified'
Location/Qualifiers

    .20
    ^organism="synthetic construct"
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|db_xref="taxon:32630"

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other sequences; artificial sequences.
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/organism="unidentified"
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26-MAR-1999 JP 2000538025
26-MAR-1998 US 09/0488:
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CQ794181.1 GI:46406823
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Mutant er g(a) and test systems for transactivation
Patent: WG 0142307-A 44 14-JUN-2001;
Sumitomo Chemical Company, Limited (JP)
Location/Qualifiers
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Luciferase expression cassettes and methods of use Patent: WO 0118195-A 12 15-WAR-2001;
Xenogen Corporation (US)
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Sequence 15 from Patent WO0208431.
AX361094
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Sequence 44 from Patent WO0142307.
20 bp
Sequence 12 from Patent WO0118195.
AX093430
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1 (bases 1 to 20)
Griffais,R., Hoiseth,S.K., Zagursky,R.J., Metcalf,B.J., Peek,J.A., Sankaran,B. and Pletcher,L.D.
Chlamydia pneumoniae polynucleotides and uses thereof
Patent: US 6559294-A 2767 06-MAY-2003;
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Francis, K.P., Contag, P.R. and Joh, D.J.
Luciferase expression cassettes and methods of use Patent: US 6737245-A 12 18 MAY-2004;
Location/Qualifiers
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Pred. No. 6.9e+05;
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Sequence 12 from patent US 6737245.
AR535425.
AR535425.1 GI:53926637
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AR312230/c
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Francis, K.P. and Purchio, A.F.
Compositions and methods for use thereof in modifying the genomes of microorganisms
Patent: WO 0208431-A 15 31-JAN-2002;
Xenogen Corporation (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-NOV-2000 JP 2000347107
ATSUSHI NAKANISHI, SHIGERU MORITA
C12N15/09, AGIK38/00, AGIK45/00, AGIR48/00, AGIP11/00, AGIP11/06,
AGIP31/04,
AGIP31/06, AGIP31/12, AGIP31/18, AGIP37/02, AGIP37/08, AGIP43/00,
C07K16/40,
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Location/Qualifiers
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synthetic construct
other sequences; artificial sequences.

1 (bases 1 to 20)
Nakanishi, A. and Morita, S.
Novel protein and DNA thereof
Patent: JP 201204480-A 9 31-JUL-2001;
TAKEDA CHEMICAL INDUSTRIES LTD
OS Artificial Sequence
PN JP 2001204480-A 9 31-JUL-2001;
PN 31-JUL-2001
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/noTe="Primer LuxA-Rev"
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n 5.1.6 Compugen Ltd. Search time 238 Seconds (without alignments)	2380332	predicted by chance to have a score of the result being printed, otal score distribution.	Description Ad250445 EST R0050 Ad36589 PCR PRIME Ad405831 Nucleic a Aac053691 Rat P2X 7 Ada09833 Antisense Aav97668 Human EGF Ad485562 Nucleic a Ad4965624 Primer of Ad550105 Human BCL Ad550105 Human BCL Ad550105 Human BCL Ad550109 Human BCL Ad450109 Human HCR Ad4707938 Human HMG Ad470331 Human MDZ Ad402331 Human MDZ
GenCore version 5. Copyright (c) 1993 - 2005 Cc OM nucleic - nucleic search, using sw model Run on: August 12, 2005, 08:59:07; Sea	Title: Perfect score: 1 Sequence: 1 ctggcgtatctgaagagtctg 21 Scoring table: 1DENTITY_NUC Gapop 10.0, Gapext 1.0 Searched: 4390206 seqs, 2959870667 residues Total number of hits satisfying chosen parameters Minimum DB seq length: 0 Maximum DB seq length: 21 Post-processing: Minimum Match 0% Maximum Match 100%	Geneseq.16Dc04:* geneseq.1900s:* geneseq.12000s:* geneseq.2001as:* geneseq.2001as:* geneseq.2001as:* geneseq.2002as:* geneseq.2003as:* geneseq.2003as:* geneseq.2003as:* geneseq.2003as:* geneseq.2003as:* than or equal to the score r than or equal to the score	Result Query Duck Duck Duck Duck Duck Duck Duck Duck

BP

ADJ85951 standard; DNA; 20

ADJ85951/c RESULT 2

(first entry)

06-MAY-2004

ADJ85951;

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Adb02332 Human MDZ
Adb02330 Human MDZ
Ad147815 Human IKK
Aaz71326 Human bia
Aav27078 Primer YA
Aaa82881 cdf4 ribo
Aaa82880 cdf4 ribo
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                                                                                                                                                                                                                                                                                              PB39; human; prostate cancer; PC; chromosome llpll.l-ll.2; cancer; prostate epithellum; splicing mechanism; early diagnosis; progression; precancerous cell; metastatic potential; non-neoplastic prostate disease; expressed sequence tag; EST; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene which is dysregulated in prostate cancer useful for diagnosing
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AAA82881
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    AAZ50445;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This invention relates to a novel DNA molecule which comprises a DNA molecule made up of the following elements in a 5' to 3' direction: a first restriction endonuclease site; a T3 promoter site; at least one Ta gene comprising at least 5 20mer Tag sequences; a Poly A site having at least 2 consecutive A residues; a second restriction endonuclease site which may be the same or different than the first restriction the T3 promoter. The invention may be useful in nucleic acid analysis, in particular to synthetic Tag genes useful as assay controls, in assay development, product development and validation and for controls.
                                                                                               restriction endonuclease site; T3 promoter site; Tag gene; Poly A site; T7 Promoter; nucleic acid analysis; synthetic Tag gene; assay control; assay development; product development; product validation; quality control; probe; ss.
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                                                                         Nucleic acid analysis-related Tag probe SeqID1019.
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Pred. No. 3.5e+03;
0; Mismatches 2;
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88.2%;
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Best Local Similarity 88.2
Matches 15; Conservative
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Unidentified.
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PCR; 88; primer; permeabilising activity; P2X7 receptor; P2Z receptor; receptor; ATP; antigen presenting cell; T lymphocyte; mitogenic stimulation; multinucleated giant cell; adenosine triphosphate; 3.-0-(4-benzoyl)benzoyl ATP; B2ATP; fluorescent dye; propidium iodide; noctropic; neuroprofective; immunosuppressive; cerebroprotective; vasotropic; arthritic disorder; respiratory disorder; neuropease; Alzheimer's disease; inflammation; rhemmatopoietic system; immune response; allergy; haematopoietic system; immune response; allergy; allymphoproliferative disorder; apoptosis; ischaemia; rat; autoimmune disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to rat and human purinergic receptor P2X 7/P2Z (AAC63693-C63694). The P2X 7 coding sequences can be used to treat disorders of the nervous system, particularly diseases with a component of chronic inflammation, such as Alzheimer's disease, diseases involving acute or chronic inflammation such as rheumatoid arthritis, of the haematopoietic system and immune response such as autoimmune of the haematopoietic system and immune response such as autoimmune disorders, allergies and lymphoproliferative disorders diseases and mirothying apoptocic cell death, such as cardiac and cerebral ischaemia and mirotobial infections, particularly tuberculosis. The present sequence is a PCR primer used to isolate the rat P2X_7 coding sequence
                                                                                                                                                                                                                                                                                                                                                                                 Mammalian purinergic receptor (P2X7) useful for screening for modulators which are useful for treating arthritic, respiratory disorders and neurodegenerative disorders, and to generate receptors specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antisense nested PCR primer #1 for amplification of rat P2X7 (P2Z).
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nes 13; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PCR primers AAZ01426-Z06209 were used to amplify open reading frames (ORFs) of the genome of Chlamydia trachomatis (see AAZ01425). These ORFs accode polypeptides (see AAY36754-Y37949) which can be used as vaccines against Chlamydia trachomatis. Antisense and ribozyme sequences can also be used to control growth of the microorganism. Chlamydia trachomatis is responsible for a large number of diseases, e.g. eye diseases such as conventional trachoma, nonendemic trachoma, paratrachoma, and inclusion conjunctivitis; genital diseases such as nongonococcal utetriis, pepidymitis, cervicitis, alpingitis, perihapatitis, bartholinitis; pneumopathy in breast feeding infants; and venereal lymphogranulomatosis. The polypeptides of the invention may be of use in treating these
                                                Vaccine, eye disease, conventional trachoma, nonendemic trachoma;
paratrachoma, inclusion conjunctivitis, genital disease, perihepatitis;
nongonococcal uretritis, epidymitis, cervicitis, salpingitis; PCR primer;
bartholinitis; pneumopathy; venereal lymphogranulomatosis; ss.
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primer used to amplify an ORF of Chlamydia trachomatis.
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Chlamydia trachomatis.
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04-NOV-1998;
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Query Match Best Loc Matches

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Gaps

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Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           THE STATE OF THE S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention discloses a method for screening a compound for its ability to modulate the permeabilising activity of a mammalian P2X7 (P2Z) receptor. The P2Z receptor is a cell surface receptor for ATP and has been implicated in the lysis of antigen presenting cells by cytotoxic T lymphocytes, in the mitogenic stimulation of human T lymphocytes, as well as in the formation of multinucleated giant cells. The preferred agonist is adenosine triphosphate (ATP) or 3'-0-(4-benzoyl)benzoyl ATP (BzATP) and the preferred method comprises monitoring the uptake into the cell of a detectable molecule, preferably a fluorescent dye (e.g. propidium iodidity to modulate the permeabilising activity of a mammalian p2X7 receptor useful for treatment of arthritic and respiratory disorders and reurodegenerative diseases. It is particularly useful in the treatment of Alzheimer's disease, diseases involving acute or chronic inflammation including rheumatoid arthritis, amyloidosis, bacterial, viral and other microbial infections, e.g. tubberculosis, disorders allergies and respiratory disorders of lymphoproliferative diseases including autoimmune disorders, allergies and such and action and an expense of presented is a particularly apoptotic cell death, and a cardiac and cerebral ischaemia. The sequence presented is a particularly appropriated the particularly apoptotic cell death, and a particular presented is a particular particular presented or a particular particular presented or a particular particula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                              Screening of compound for its ability to modulate permeabilizing activity of mammalian receptor useful for treating e.g. arthritis, and alzheimer's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human, epidermal growth factor receptor; EGFR; EGF-R; target sequence;
hammerhead ribozyme; hairpin ribozyme; inhibition; cell proliferation;
cancer; genetic drift; detection; mutation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nested PCR primer used for the amplification of rat P2X7 cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61.9%; Score 13; DB 9; Length 20; 100.0%; Pred. No. 9e+03; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human EGF-R target sequence nucleotide position 3858.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 20 BP; 4 A; 3 C; 7 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; SEQ ID NO 3; 43pp; English
                                                                                                                                                                                            Kawashima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 '668/c
AAV97668 standard; RNA; 17 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97US-0036476P.
97US-00985162.
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                         15-AUG-2000; 2000US-00638857
                                                                                 28-APR-1997; 97US-00842079
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 GGCGTATCTGAAG 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GCCGTATCTGAAG 13
                                                                                                                                                                                            Surprenant A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13; Conservative
                                                                                                                                 (GLAX ) GLAXO GROUP LTD
                                                                                                                                                                                                                                              WPI; 2003-502654/47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9833893-A2
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04-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-AUG-1998
                                                                                                                                                                                         Buell GN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAV97668;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                         disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New DNA molecules made by annealing and extending overlapping 60mer oligonuclectides, useful in producing synthetic Tag genes useful as assay controls, in assay development, product development and for quality
                                                                                                                                                                                                                                   tic nucleic acids - which cleave RNA derived from an epidermal factor receptor, useful for inhibiting cell proliferation and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     restriction endonuclease site; T3 promoter site; Tag gene; Poly A site; T7 Promoter; nucleic acid analysis; synthetic Tag gene; assay control; assay development; product development; product validation; quality control; probe; 8s.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61.0%; Score 12.8; DB 2; Length 17; 87.5%; Pred. No. 1.1e+04; Live 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seguence 17 BP; 4 A; 6 C; 2 G; 0 T; 5 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acid analysis-related Tag probe SeqID630.
                                                                                                            Mcswiggen JA;
                                                                                                                                                                                                                                                                                                                                                                                    Claim 5; Page 77; 109pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-JUL-2002; 2002US-0395530P.
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(RIBO-) RIBOZYME PHARM INC
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Best Local Similarity 87...
Best Local 14; Conservative
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                                                                                                                                                                                                                                              Enzymatic nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (AFFY-) AFFYMETRIX INC.
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                                                                                                                                                                          WPI; 1998-437449/37
                                                                                                        Fell P,
                                    (UYAS-) UNIV ASTON
                                                                                                                                                                                                                                                                                                                   treating cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO2004007684-A2.
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ADF50105
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                                    This invention relates to a novel DNA molecule which comprises a DNA molecule made up of the following elements in a 5' to 3' direction: a first restriction endonuclease site; a T3 promoters site; at least on Tag gene comprising at least 5 20mer Tag sequences; a Poly A site having at least 2 consecutive A residues; a second restriction endonuclease site which may be the same or different than the first restriction endonuclease site endonuclease site; or a T7 Promoter on the opposite strand as the T3 promoter. The invention may be useful in nucleic acid analysis, in particular to synthetic Tag genes useful as assay controls, in assay development, product development and validation and for quality control. The present sequence is that of a Tag oligonucleotide probe which may be used during the creation of the novel DNA molecule of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to a polynucleotide isolated from a human gene and is useful for detecting a single nucleotide polymorphism in a human gene or for diagnosing of disease. The invention enables the detection of a single nucleotide polymorphism in a human gene. The
                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel polynuclectide useful for PCR amplification along with two fragment from another set of sequences, or for detecting single nuclectide polymorphism in human gene.
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                                                                                                                                                                                                                                                         61.0%; Score 12.8; DB 12; Length 20; 87.5%; Pred. No. 1.1e+04;
                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human; single nucleotide polymorphism; SNP; ss; primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        present sequence represents a primer of the invention.
                                                                                                                                                                                                                                                                     Pred. No. 1.1e+04;
0; Mismatches 2;
                                                                                                                                                                                                                               Sequence 20 BP; 5 A; 4 C; 6 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 20 BP; 5 A; 3 C; 8 G; 4 T; 0 U; 0 Other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 2; SEQ ID NO 5283; 2627pp; Japanese.
               Disclosure; SEQ ID NO 630; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Primer of the invention #1974.
                                                                                                                                                                                                                                                                                                                                                                                                                        ADK96254 standard; DNA; 20 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-MAR-2002; 2002JP-00064373.
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                                                                                                                                                                                                                                                                                                                                       17 GCGTATCTGCATAGTC 2
                                                                                                                                                                                                                                                                                                                       4 GCGTATCTGAAGAGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                         14; Conservative
                                                                                                                                                                                                                                                                             Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADK96254;
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Best Local S
                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                          Matches
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The invention relates to a novel short interfering nucleic acid (siNA) that downregulates expression of the BCL2 gene by RNA interference. A siNA of the invention has cytostatic, immunosuppressive, virucide, and anti-HIV activity. The siNA are useful for modulation (inhibition) of expression or activity of BCL2 by RNA interference. siNA are used to modulate expression of BCL2 genes, in cells, tissue explants or organisms, e.g. for treating cancer, autoimmune diseases and viral infections (including by HIV) but also for drug screening, diagnosis, target identification and validation, genetic engineering, pharmacogenomics, studying gene function and gene mapping (e.g. of single runclectide polymorphisms). The sequences shown in ADF49273-ADF50143 represent siNA of the invention.
                                                                                                                                                                                                               ss; siNA; human; BCL2; short interfering nucleic acid; RNA interference; cytostatic; immunosuppressive; virucide; anti-HIV; cancer; autoimmune disease; viral infection; HIV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New short interfering nucleic acid, useful e.g. for treatment and diagnosis of cancer or autoimmune disease, downregulates expression of the BCL2 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 21 BP; 3 A; 5 C; 5 G; 2 T; 6 U; 0 Other;
                                                                                                                                                              Human BCL2 siNA target sequence SEQ ID NO:833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 3; SEQ ID NO 833; 148pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; 2002US-0396905P.
; 2002US-0406784P.
; 2002US-0408378P.
; 2002US-0409293P.
ADF50105 standard; RNA; 21 BP
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2002US-0386782P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (RIBO-) RIBOZYME PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mcswiggen J, Beigelman L;
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4 GUCUCUGAAGACUCUG
                                                                                                          (first entry)
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29-AUG-2002;
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                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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                                                      ADF50105;
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ADF50117/C
ID ADF50
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1 CTGGCGTATCTGAAGA 16

Matches

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ADF50117;

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ss; siNA; human; BCL2; short interfering nucleic acid; RNA interference; cytostatic; immunosuppressive; virucide; anti-HIV; cancer; autoimmune disease; viral infection; HIV.
            ss; siNA; human; BCL2; short interfering nucleic acid; RNA interference; cytostatic; immunosuppressive; virucide; anti-HIV; cancer; autoimmune disease; viral infection; HIV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a novel short interfering nucleic acid (siNA) that downregulates expression of the BCL2 gene by RNA interference. A siNA of the invention has cytostatic, immunosupressive, virucide, and anti-HIV activity. The siNA are useful for modulation (inhibition) of expression or activity of BCL2 by RNA interference. siNA are used to modulate expression of BCL2 genes, in cells, tissue explants or organisms, e.g. for treating cancer, autoimmune diseases and viral infections (including by HIV) but also for drug screening, diagnosis, target identification and validation, genetic engineering, pharmacogenomics, studying gene function and gene mapping (e.g. of sing represent siNA of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New short interfering nucleic acid, useful e.g. for treatment and diagnosis of cancer or autoimmune disease, downregulates expression of the BCL2 gene.
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87.5%; Pred. No. 1.2e+04;
tive 0; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human BCL2 siNA target sequence SEQ ID NO:837.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 3; SEQ ID NO 853; 148pp; English.
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2002US-0363124P.
2002US-0386782P.
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2002US-0406784P.
2002US-0408378P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      (RIBO-) RIBOZYME PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mcswiggen J, Beigelman L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTATCTGAAGAGTCTG
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Best Local Similarity 87.5
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-712622/67.
                                                                                                                                   WO2003070969-A2
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                                                                                                Homo sapiens
                                                                                                                                                                                                                                                         20-FEB-2002;
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06-JUN-2002;
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                                                                                                                                   88; 8iNA; human, BCL2; short interfering nucleic acid; RNA interference; cytostatic; immunosuppressive; virucide; anti-HIV; cancer; autoimmune disease; viral infection; HIV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New short interfering nucleic acid, useful e.g. for treatment and diagnosis of cancer or autoimmune disease, downregulates expression of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 21 BP; 6 A; 5 C; 5 G; 2 T; 3 U; 0 Other;
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                                                                                            Human BCL2 sinA target sequence SEQ ID NO:845.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 3; SEQ ID NO 845; 148pp; English.
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; 2002US-0386782P.
; 2002US-0396905P.
; 2002US-0406784P.
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2002US-0409293P.
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                                                       (first entry)
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Best Local Similarity
                                                                                                                                                                                                                                                         WO2003070969-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the BCL2 gene.
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                                                                                                                                                                                                                    Homo sapiens.
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06-JUN-2002;
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29-AUG-2002;
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ADF50125,

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The invention relates to a double-stranded short interfering nucleic acid

(siNA) molecule that down-regulates expression of an endogenous mammalian

target gene comprising one or more chemical modifications and each strand

of the double-stranded siNA comprises about 21 nucleotides. The siNA of

the invention demonstrates antiarteriosclerotic, neuroprotective,

che invention demonstrates antiarteriosclerotic, neuroprotective,

contropic, antiparkinsonian and anticonvulsant activities and may be

useful for down-regulating the expression of an endogenous mammalian

target gene and therefore in the treatment of any disease or condition

target gene and therefore in the treatment of any disease or condition

target gene and therefore in the treatment of any disease or condition

tissue or organism. The disease or condition may include pulmonary

diseases such as restenosis, atherosclerosis, Alzheimer's disease or

Parkinson's disease, epilepsy, dementia, huntington's disease or

Parkinson's disease, epilepsy, dementia, huntington's disease or

amyotropic lateral sclerosis. Furthermore, the siNA may be utilised for

gene therapy applications. The current sequence is that of the siNA DNA-
                                                                                                                                                                                                                                                                                                                                                                                                                                New double-stranded short interfering nucleic acid molecule, useful for down-regulating the expression of an endogenous mammalian target gene or for treating diseases that respond to modulation of gene expression or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antiarteriosclerotic; neuroprotective; nootropic; antiparkinsonian; anticonvalsant; pulmonary disease; restenosis; atherosclerosis; Alzheimer's; Parkinson's; epilepsy; dementia; huntington's; amyotrophic lateral sclerosis; gene therapy; ss; DNA-RNA hybrid; BCL2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61.0%; Score 12.8; DB 10; Length 21; 56.2%; Pred. No. 1.2e+04; vative 5; Mismatches 2; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   double-stranded short interfering nucleic acid; siNA;
                                                                                                                                                                                                                                                                                                                    Chowrira B, Pavco P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 21 BP; 3 A; 5 C; 5 G; 2 T; 6 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                              Thompson J;
                                                                                                                                                                                                                                                                           (SIRN-) SIRNA THERAPEUTICS INC
                                                                                    2002US-0358580P.
2002US-0363124P.
2002US-0386782P.
2002US-0406784P.
2002US-0408378P.
2002US-0409293P.
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GUCUCUGAAGACUCUG 19
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                                           20-FEB-2003; 2003WO-US005028
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nes 9, Conservative
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                                                                                         20-FEB-2002;
                                                                                                            11-MAR-2002;
                                                                                                                                                          29-AUG-2002;
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12-SEP-2003
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a novel short interfering nucleic acid (siNA) that downregulates expression of the BCL2 gene by RNA interference. A salkA of the invention has cytostatic, immunosuppressive, virucide, and anti-HIV activity. The siNA are useful. for modulate on (inhibition) of expression or activity of BCL2 by RNA interference. siNA are used to organisms, e.g. for treating cancer, autoimmune diseases and viral infections (including by HIV) but also for drug screening, diagnosis, traget identification and validation, genetic engineering, pharmacogenomics, studying gene function and gene mapping (e.g. of single-nucleotide polymorphisms). The sequences shown in ADF49273-ADF50143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New short interfering nucleic acid, useful e.g. for treatment and diagnosis of cancer or autoimmune disease, downregulates expression of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                double-stranded short interfering nucleic acid; siNA; antiarteriosclerotic; neuroprotective; nootropic; antiparkinsonian; antionvulannt; pulmonary disease; restenosis; atherosclerosis; Alzheimer's; Parkinson's; epilepsy; dementia; huntington's; amyotrophic lateral sclerosis; gene therapy; ss; DNA-RNA hybrid; BCL2.
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    increorine polymorphisms). The irepresent sinh of the invention.

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06-JUN-2002; 2002US-0386782P.

18-JUL-2002; 2002US-0396905P.

29-AUG-2002; 2002US-0406784P.

05-SEP-2002; 2002US-0408378P.

09-SEP-2002; 2002US-0408378P.
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                                                                                                                                                                                                                                                                                                                                                                                                                    Beigelman L;
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Best Local Similarity 87.5
Matches 14; Conservative
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RESULT 13 ADG29696

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(SIRN-) SIRNA THERAPEUTICS INC.
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2002US-0408378P.
2002US-0409293P.
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2002US-0386782P.
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tes 14; Conserv
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RNA interference.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO2004045543-A2.
WO2003074654-A2.
                                                                                                                                                                                                                                                                               Mcswiggen J,
Jamison S, L
                                                                                                                                                           29-AUG-2002;
                                                                                                                                                                           05-SEP-2002;
                                                                                                                                                                                           09-SEP-2002;
                                                                                                                                                                                                              15-JAN-2003;
                                                                                                       20-FEB-2002;
                                                                                                                          11-MAR-2002;
                                                                                                                                        06-JUN-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03 - JUN - 2004
                                  12-SEP-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADQ61043;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADQ61043/
BXBXBXBXBXC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a double-stranded short interfering nucleic acid (siNA) molecule that down-regulates expression of an endogenous mammalian target gene comprising one or more chemical modifications and each strand of the double-stranded siNA comprises about 21 nucleotides. The siNA of the invention demonstrates antiatreriosclerotic, neuroprotective, notiparkinsonian and anticonvulsant activities and may be neeful for down-regulating the expression of an endogenous mammalian target gene and therefore in the treatment of any disease or condition target gene and therefore in the treatment of any disease or condition target sense and may see that responds to modulation of gene expression or activity in a cell, tissue or organism. The disease or condition may include pulmonary diseases such as restenosis, atherosoclerosis, Alzheimer's disease, Parkinson's disease, epilepsy, dementia, huntington's disease or parkinson's disease or condition and parkinson's disease or sentencesis. Furthermore, the siNA may be utilised for gene therapy applications. The current sequence is that of the siNA DNA-RNA hybrid of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                               New double-stranded short interfering nucleic acid molecule, useful for down-regulating the expression of an endogenous mammalian target gene or for treating diseases that respond to modulation of gene expression or activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             double-stranded short interfering nucleic acid; siNA; antiarteriosclerotic; neuroprotective; nootropic; antiparkinsonian; antioorulaant; pulmonary disease; restenosis; atherosclerosis; Alzheimer's; Parkinson's; espilepsy; dementia; huntington's; amyotrophic lateral sclerosis; gene therapy; ss; DNA-RNA hybrid; BCL2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                   Fosnaugh K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61.0%; Score 12.8; DB 10; Length 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 1.2e+04;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                   Pavco P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 21 BP; 6 A; 5 C; 5 G; 2 T; 3 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BCL2-targeted sina DNA-RNA hybrid - SEQ ID 266.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 24; SEQ ID NO 259; 593pp; English.
                                                                                                                                                                                                                                                                 Chowrira B,
                                                                                                                                                                                                                                                                                 Usman N, Thompson J;
                                                                                                                                                                                                                                (SIRN-) SIRNA THERAPEUTICS INC
                                                                                     2002US-0358580P.
2002US-0363124P.
2002US-0386782P.
2002US-0406784P.
2002US-0406378P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADG29700 standard; RNA; 21 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21
                                                                                                                                                                                               2003US-0440129P
                                                      20-FEB-2003; 2003WO-US005028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 Similarity 87.5%;
14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16 GTCTCTGAAGACTCTG 1
                                                                                                                                                                                                                                                                   Beigelman L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 GTATCTGAAGAGTCTG
                                                                                                                                                                                                                                                                                                                      WPI; 2003-731676/69.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
                                                                                                                                          29-AUG-2002; 2
05-SEP-2002; 2
09-SEP-2002; 2
                                                                                                                                                                                               15-JAN-2003;
                                                                                                                                                                                                                                                                    Mcswiggen J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unidentified
                                                                                                                            06-JUN-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-FEB-2004
                    12-SEP-2003
                                                                                                                                                                                                                                                                                     Jamison S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADG29700;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 15
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The invention relates to a double-stranded short interfering nucleic acid (siNA) molecule that down-regulates expression of an endogenous mammalian target gene comprising one or more chemical modifications and each strand of the double-stranded siNA comprises about 21 nucleotides. The siNA of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the invention demonstrates animarcus and autocorrective, neuroprotective, nootropic, antiparkinsonian and anticonvulsant activities and may be useful for down-regularing the expression of an endogenous mammalian target gene and therefore in the treatment of any disease or condition that responds to modulation of gene expression or activity in a cell, itsue or organism. The disease or condition may include pulmonary diseases such as restenosis, atherosclerosis, Alzheimer's disease, Parkinson's disease, epilepsy, dementia, huntington's disease or gene therapy applications. The current sequence is that of the siNA DNA-RNA hybrid of the invention.
                                                                                                                                                                                                                            New double-stranded short interfering nucleic acid molecule, useful for down-regulating the expression of an endogenous mammalian target gene or for treating diseases that respond to modulation of gene expression or activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            siRNA; gene silencing; Bcl-2; optimised; short interfering RNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
Beigelman L, Chowrira B, Pavco P, Fosnaugh K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61.0%; Score 12.8; DB 10; Length 21; llarity 87.5%; Pred. No. 1.2e+04; Conservative 0; Mismatches 2; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Anti-FRK siRNA related DNA sequence SEQ ID NO:745.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 21 BP; 6 A; 5 C; 5 G; 2 T; 3 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 24; SEQ ID NO 266; 593pp; English.
                                                          Thompson J;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a novel method for selecting siRNA (short interfering RNA) comprising selecting an siRNA molecule of 19-25 cucleoside bases by selecting a target gene and measuring the rule.

Cucleoside bases by selecting a target gene and measuring the cfunctionality of sequences of 19-25 nucleotides in length that are substantially complementary to a stretch of nucleotides of the target secrific criteria. Also claimed are methods for gene-silencing, developing an criteria. Also claimed are methods for gene-silencing, developing an siRNA algorithm for selecting siRNA, selecting an siRNA with improved cucle functionality, selecting siRNA, selecting an siRNA wilectle comprising the siRNA. The siRNA molecule comprises a sequence substantially similar to a sequence consisteing of GGGAGAUGAUGAUGAUGAUGA, in siRNA molecule comprises a sense strand GAGACUCUGCUCGUUGAUUC, CAUGCGCCUCUGUUGA, undexaduga, GAGAUGAUGAUGAUGAUGAUGAGUGAUGAAGUGAUGAAGUGACGAGAGUA, in the siRNA molecule comprises a sense strand and an anti-sense strand. The siRNA molecule comprises a hairpin. The siRNA molecule comprises between 18 and 30 base comprises a hairpin. The siRNA molecule comprises between 18 and 30 base siRNA and a second optimised siRNA, The method is useful in selecting siRNA for generating a gene silencing reagent. The present sequence is siRNA to remerating a gene silencing respan.
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                                                                                                                                                                                                                                                                                       Selecting siRNA by selecting an siRNA molecule of 19-25 nucleoside bases by selecting a target gene and measuring the functionality of the nucleotide sequences that are complementary to a stretch of nucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HMG-CoA reductase; 3-hydroxy-3-methylglutaryl-Coenzyme A;
HMG-CoA reductase; cardiant; antiarteriosclerotic; antilipaemic;
antisense gene therapy; cardiovascular disorder; cholesterol metabolism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human HMG-CoA reductase antisense oligonucleotide, SEQ ID No 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59.0%; Score 12.4; DB 12; Length 19; 92.9%; Pred. No. 1.88+04; tive 0; Mismatches 1; Indels
                                                                                                                                                                                              Stephen S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the specification as DNA, but described as siRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 19 BP; 7 A; 4 C; 2 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                           Devin L, William M,
                                                                                                                                                                                                                                                                                                                                                                                                                   Example 12; SEQ ID NO 745; 199pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ВР
                         14-NOV-2003; 2003WO-US036787.
                                                                    14-NOV-2002; 2002US-0426137P.
10-SEP-2003; 2003US-0502050P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADI79541 standard; DNA; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8 ATCTGAAGAGTCTG 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 92.9
Matches 13; Conservative
                                                                                                                                                                                              Anastasia K, Angela R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18 ATATGAAGAGTCTG
                                                                                                                                                                                                                                                                                                                                                                        of the target sequence.
                                                                                                                                                (DHAR-) DHARMACON INC
                                                                                                                                                                                                                                            WPI; 2004-420527/39.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-APR-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADI 79541;
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XX
AC ADI7
XX
XX
YX
XX
YX
XX
XX
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XW
HMG

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The invention relates to novel compounds of 8-80 nucleobases in length targeted to, and which specifically hybridises with, a nucleic acid molecule encoding 3-hydroxy-3-methylgulatry-1-Comaryme A (HMG-COA) compounds have cardiant, antiarteriosclerotic, and antilipaemic activities. The compounds can be used to treat disorders by antisense gene therapy. The compounds, compositions and methods are useful for treating a disease or condition associated with HMG-COA reductase, such as a cardiovascular disorder e.g. atherosclerosis, or a disease or condition involving cholesterol metabolism. They are also useful in research and diagnostics for modulating the expression of HMG-COA reductase. This polymucleotide sequence represents an antisense oligonucleotide of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HMG-CoA reductase; 3-hydroxy-3-methylglutaryl-Coenzyme A;
HMG-CoA reductase; cardiant; antiarteriosclerotic; antilipaemic;
antisense gene therapy; cardiovascular disorder; cholesterol metabolism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                New compounds, particularly antisense oligonucleotides targeted to nucleic acid encoding HMG-CoA reductase, useful for treating atherosclerosis, or a disease involving cholesterol metabolism or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 12.4; DB 12;
Pred. No. 1.8e+04;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 20 BP; 5 A; 3 C; 7 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 15; SEQ ID NO 64; 110pp; English.
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0
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                                                                                                                                                                                 Dobie KW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BP.
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02-JUL-2002; 2002US-00190366.
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                                                         02-JUL-2002; 2002US-00190366.
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ID ADI79738 standard; DNA; 20
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Best Local Similarity 92.9
Matches 13; Conservative
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                                                                                                                     (ISIS-) ISIS PHARM INC.
                                                                                                                                                                                 Freier SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dean NM, Freier SM,
                                                                                                                                                                                                                                       WPI; 2004-081743/08.
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                                                                                                                                                                                                                                                                                                                                                                                                   angiogenesis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-JAN-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AD179738;
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                                                                                                                                                                                 Dean NM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 18
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The invention relates to novel compounds of 8-80 nucleobases in length targeted to, and which specifically hybridises with, a nucleic acid molecule encoding 3-hydroxy-3-methylglutaryl-Consyme A (HMG-COA) reductase, and inhibits the expression of HMG-COA reductase. The novel compounds have cardiant, antiarteriosclerotic, and antilipaemic activities. The compound can be used to treat disorders by antisense gene therapy. The compounds, compositions and methods are useful for treating a disease or condition associated with HMG-COA reductase, such as a cardiovascular disorder e.g. atherosclerosis, or a disease or condition involving cholesterol metabolism. They are also useful in research and diagnostics for modularing the expression of HMG-COA reductase. This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes enzymatic nucleic acid molecules (NAMs) which specifically cleave RNA derived from an epidermal growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; epidermal growth factor receptor; EGFR; EGF-R; target sequence;
hammerhead ribozyme; hairpin ribozyme; inhibition; cell proliferation;
cancer; genetic drift; detection; mutation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Enzymatic nucleic acids - which cleave RNA derived from an epidermal growth factor receptor, useful for inhibiting cell proliferation and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                       New compounds, particularly antisense oligonucleotides targeted to nucleic acid encoding HMG-COA reductase, useful for treating atherosclerosis, or a disease involving cholesterol metabolism or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59.0%; Score 12.4; DB 12; Length 20; 92.9%; Pred. No. 1.8e+04; ive 0; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human EGF-R target sequence nucleotide position 3859.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seguence 20 BP; 5 A; 7 C; 3 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                          Example 16; SEQ ID NO 261; 110pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mcswiggen JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAV97669 standard; RNA; 17 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98WO-US000730.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
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                                                                                                                                angiogenesis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAV97669;
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The present invention relates to novel human zinc finger-containing proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is encoded at chromosome 742.1, MD24 is encoded at chromosome 6p21.3-22.2, MD27 is encoded at chromosome 6p21.3-22.2, mD27 is encoded at chromosome 6p21.3 sequences are useful in therapy, or in manufacturing a medicament for treating or preventing a disorder associated with decreased or increased expression or activity of MD23, MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic acids and proteins are also useful for diagnosing or monitoring a disease caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic acids can also be used as probes to detect and characterize gross alterations in MD23, MD24, MD27, or MD212. The probes are useful in constructing microarrays for measuring gene expression. The proteins are useful as therapeutic agents for gene therapy or as
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receptor (EGF-R) gene. AAV97221 to AAV98043 and AAV98979 to AAV99090 represent specifically claimed target sequence from human EGF-R. AAV98044 to AAV98865 and AAV98865 to V9878 represent hammershead ribozymes and hairpin ribozymes respectively for human EGF-R. The NAMS are useful for cleaving EGF-R RNA in the treatment of a condition associated with EGFR expression levels e.g. to inhibit cell proliferation in the prevention or treatment of cancers. The NAMS can also be used as diagnostic tools to examine genetic diift and mutations within diseased cells or to detect the presence of EGF-R RNA in a cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cytostatic; immunostimulant; gene therapy; vaccine; human; zinc finger protein; MDZ3; MDZ4; MDZ12; MDZ12; chromosome 7q22.1; chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer; developmental disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New zinc finger-containing proteins and nucleic acids, useful in manufacturing a medicament for treating or preventing a disorder associated with decreased or increased expression or activity of MDZ3,
                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                     58.1%; Score 12.2; DB 2; Length 17; 82.4%; Pred. No. 2.3e+04; ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                   Sequence 17 BP; 4 A; 6 C; 2 G; 0 T; 5 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human MDZ4 scanning oligonucleotide SEQ ID 3317.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MDZ4, MDZ7 or MDZ12, e.g. cancer.
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                                                                                                                                                                                                                                                                                                                                            4 GCGTATCTGAAGAGTCT
                                                                                                                                                                                                                                                                                                                                                                                  GGGTATCGAAAGAGTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADB02331 standard; DNA; 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-NOV-2003 (first entry)
                                                                                                                                                                                                                                                                                                      14; Conservative
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                                                                                                                                                                                                                                                                                  Local Similarity
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                                                                                                                                                                                                                                                               Query Match
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Isolated Kaposi's sarcoma-associated herpesvirus proteins - comprising antigenic membrane protein, G protein coupled receptor and cyclin protein used to develop products for diagnosis and therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The sequence is that of a 3' PCR primer P16 which was used to detect transcripts of ORF73 of Kaposi's sarcoma herpesvirus (KSHV). (Updated on 27-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58.1%; Score 12.2; DB 2; Length 20; 82.4%; Pred. No. 2.3e+04; Live 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                 Kaposi's sarcoma associated herpesvirus ORF73 PCR primer.
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                                                                                                                                                                                                                                                                                                          PCR primer; KSHV; ORF73; Kaposi's sarcoma; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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                                                     AAV31711 standard; DNA; 20 BP
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                                                                                                                                                                    (revised)
                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
Human herpesvirus 8.
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Synthetic.
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11-SEP-1998
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                                                                                                           AAV31711;
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AAD61207/c
ID AAD612
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Matches
RESULT 22
                    AAV3171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kaposi's sarcoma-associated herpes virus positive cell lines - comprising Kaposi's sarcoma-associated herpes virus, used to study virus and to develop diagnostic and therapeutic products.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PCR primers AAV29902-03 were used to amplify open reading frame (ORF) 73 of Kaposi's sarcoma-associated herpes virus (KSHV). The specification describes a cell line comprising KSHV, the cell line preferably being a body cavity-based lymphoma cell line that does not harbour the Epstein-Barr virus. The KSHV cell lines can be used for the characterisation of the properties and functions of the infectious agent KSHV. The purified virus can be used for diagnostic purposes, e.g. for the detection of antibodies which can be used for diagnostic and/or treatment purposes. (Updated on 27-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KSHV; body cavity-based lymphoma cell line; Epstein-Barr virus;
characterisation; diagnosis; detection; antibody treatment; PCR primer;
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                                                                                                                                                                          Gaps
vaccines. The present sequence was used to illustrate the invention
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                                                                                                     ch 58.1%; Score 12.2; DB 8; Length 17; I Similarity 82.4%; Pred. No. 2.3e+04; 14; Conservative 0; Mismatches 3; Indels
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                                                        Sequence 17 BP; 5 A; 6 C; 2 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mesri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3' PCR primer used to amplify the KSHV ORF 73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arvanitakis L, Knowles DM,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CORR ) CORNELL RES FOUND INC.
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(first entry)
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Best Local Similarity
Matches 14; Conserv
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Human herpesvirus
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06-AUG-1998
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Best Local S
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17-SEP-2002; 2002WO-IB004523.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       acid molecule encoding Ship-1 (also known as SH2-containing phosphatidylinositol phosphatase-1 and INPPSD) to modulate/inhibit the expression of Ship-1. The invention is useful in treatment of diseases such as insensitivity to apoptotic signals, autoimmune disorders, developmental disorders and inflammatory disorders. The present sequence is human Ship-1 antisense oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antisense therapy, human, interleukin-1 receptor-associated kinase-1; IL-1 receptor-associated kinase-1; IRAK-1; hyperproliferative disorder e.g.; cancer; autoimmune disorder; alterative disorder infiammation; cytostatic; immunosuppressive; osteopathic; antiinflammatory; phosphorothioate; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       present invention provides antisense compounds targetted to nucleic
note= "Phosphorothioate backbone; All cytidines are 5-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antisense compounds targeted to nucleic acid molecule encoding Ship-1, useful for treating diseases associated with expression of Ship-1, sucas autoimmune and developmental disorders.
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/note= "This oligonucleotide has a phosphorothioate
                                                                                                                                           *tag= c
/mod_base= OTHER
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                                                                                                    nucleotides"
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                                                                             "mod_base= OTHER
'note= "2'-0-methoxyethyl (2'-MOE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 20 BP; 6 A; 7 C; 4 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human IRAK-1 DNA, antisense oligonucleotide #65.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                      methyl cytidines
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                                                                                                                                                                                                                                                                                                                                                                                                                      Freier SM;
                                                               *tag=
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Best Local Similarity
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The present invention relates to antisense compounds targeted to a nucleic acid encoding interleukin-1 (IL-1) receptor-associated kinase-1 (IRA-1). The antisense compound comprises an antisense oligonucleotide that specifically hybridises with the nucleic acid and inhibits the expression of IRAK-1. The antisense oligonucleotide is a chimeric oligonucleotide. The antisense oligonucleotide is a chimeric comprises at least one modified super modely a phosphorothicate linkage. It also comprises at least one modified sugar moiety, preferably a 2'-0-methoxyethyl (2'-MOE) sugar moiety. The antisense oligonucleotide further comprises at least one modified nucleobase, preferably a 2'-0-methoxyethyl (2'-MOE) sugar moiety. The antisense oligonucleotide further comprises at least one modified nucleobase, preferably a 5'-0-methoxyethyl classes such as hyperproliferative disorders, e.g. cancer, autoimmune disorders, altered bone metabolism, and inflammation. The presents sequence represents an antisense oligonucleotide used in the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New compound having a sequence targeted to a nucleic acid encoding IL-1 receptor-associated kinase-1, useful for preparing a composition for treating hyperproliferative or autoimmune disorder or inflammation.
backbone and 2'-methyoxyethyl (2'-NOE) wings at the 5' and 3' ends, which are 5 nucleotides in length at each end. All cytidine residues are 5-methylcytidines"
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82.4%; Pred. No. 2.3e+04;
live 0; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dobie KW;
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hes 14; Conservative
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(ISIS-) ISIS PHARM INC.
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                       Bennett CF,
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                                                                                                                                                                                                   in the phenomena of tumour suppression, tumour reversion, appropriate and/or resistence to viruses. The invention may be useful for the development of compounds with a cytostatic, virucide, neuroprotective, nootropic or neuroleptic activity. The DNA sequences may be useful as probes and primers for detecting, indentifying, quantifying and/or cample as one component of a gene chip, in virto as antisense reagents and for production of recombinant polypeptides. The invention may therefore be useful for preparation of polypeptides. The invention and/or treatment of viral diseases that are characterised by development of tumours or cell degeneration, specifically cancer but also Alzheimer's disease and schizophrenia. The preparent sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human nucleolin phosphorothioate antisense oligonucleotide, SEQ ID NO:73.
                                                                                                               New isolated nucleic acid, useful for treating viral diseases associated with tumors and cell degeneration, also related polypeptides, antibodies
                                                                                                                                                                                           This invention relates to novel isolated nucleic acid sequences involved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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100.0%; Pred. No. 2.9e+04;
.ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 17 BP; 6 A; 4 C; 2 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                       ftp.wipo.int/pub/publishedpct_sequences
                                                                                                                                                                  Disclosure; SEQ ID NO 3472; 30pp; French.
                                                              Tuijnder M;
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                                      (MOLE-) MOLECULAR ENGINES LAB.
              17-SEP-2001; 2001FR-00011980.
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                                                                                                                             with tumors and cell dand transfected cells.
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                                                              Amson R,
                                                                                      WPI; 2003-313354/30.
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                                                               Telerman A,
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Sequences AAC92560-C92639 represent antisense oligonucleotides targetted to the human nucleolin gene, which inhibit its expression. The antisense oligonucleotides were designed to target different respions of the human nucleolin menals and were analysed for their effect on nucleolin mRNA and were analysed for their effect on nucleolin mRNA concleolin mRNA, and were analysed for their effect on nucleolin mRNA concleolin primarily participates in ribosome biogenesis and confidence in the nucleolin primarily participates in ribosome biogenesis and confidence in the nucleolus via a ribonucleoprotein consensus sequence. Thosomes in the nucleolus via a ribonucleoprotein consensus sequence. Thosomes in the nucleolus via a ribonucleoprotein consensus sequence. Thosomes in the randduction, and chromatin decondensation. Nucleolus correspication, signal transduction, and chromatin decondensation. Nucleolus is a member of the Ag-NOR (active ribosomal gene located in the nucleolar corputation, signal transduction, and chromatin decondensation nucleolar corputation family of proteins which are markers of active corputates and whose expression is associated with the predence connective tissue diseases such as systemic connective tissue diseases such as the oligonucleotides of the invention are useful for diagnosis, corputation and treatment of conditions associated with nucleolin corputation, such as tumour formation, immune disorders and inflammation
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                                                                                  Novel antisense compound targeted to human nucleolin which specifically hybridizes with and inhibits the expression of human nucleolin, useful for modulating the expression of nucleolin in cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seguence 20 BP; 5 A; 6 C; 2 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                  Claim 14; Col 43-44; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 TGGCGTATCTGAAGAGTCTG 21
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atches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .(ISIS-) ISIS PHARM INC
WPI; 2001-079848/09.
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AAA46172,
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                                                                                                                                                                                                                                                              targeted to a nucleic acid empoding PARR-alpha (peroxisome proliferator-activated receptor-alpha), that specifically hybridises with the nucleic acid encoding PPAR-alpha comprising 86001-bp sequence and inhibiting the expression of PPAR-alpha. Also described are: a method of inhibiting the expression of PPAR-alpha in cells or tissues; a method of screening for a modulator of PPAR-alpha in cells or tissues; a method of screening for a modulator of PPAR-alpha in cells or tissues; a method of screening for a state; a kit or assay device comprising the compound; and a method of treating an animal having a disease or condition associated with PPAR-alpha in alpha. The oligonuclectide compound is useful for preparing a composition for treating hyperproliferative disorder e.g. cancer. This sequence represents a human peroxisome proliferator-activated receptor-alpha (PPAR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention describes a compound, having a sequence comprising 8-80 bp targeted to a nucleic acid encoding PPAR-alpha (peroxisome proliferator-
                                                                                                                                                                                                                                             The invention describes a compound, having a sequence comprising 8-80 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             peroxisome proliferator-activated receptor-alpha; PPAR-alpha modulator; PPAR-alpha associated disorder; hyperproliferative disorder; human; antisense oligonucleotide; antisense technology; ss.
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                                                                               New oligonucleotide compound that inhibits expression of PPAR-alpha,
                                                                                                     for preparing a composition for treating hyperproliferative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human PPAR-alpha antisense oligonucleotide segid 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57.1%; Score 12; DB 12; L
100.0%; Pred. No. 2.9e+04;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seguence 20 BP; 6 A; 4 C; 4 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 16; SEQ ID NO 184; 121pp; English.
                                                                                                                                                                                       Example 15; SEQ ID NO 29; 121pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cytostatic; gene therapy; PPAR-alpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -alpha) antisense oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADP68748 standard; DNA; 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 TATCTGAAGAGT 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TATCTGAAGAGT 9
                                                                                                                                       disorders, e.g. cancer.
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                      WPI; 2004-449378/42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
nes 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US2004115637-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-SEP-2004
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Matches
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                        acid encoding PPAR-alpha comprising 86001-bp sequence and inhibits expression of PPAR-alpha comprising 86001-bp sequence and inhibiting the expression of PPAR-alpha. Also described are: a method of inhibiting the expression of PPAR-alpha; nealso or tissues; a method of screening for a modulator of PPAR-alpha; a diagnostic method for identifying a disease state; a kit or assay device comprising the compound; and a method of treating an animal having a disease or condition associated with PPAR-alpha; the oligonucleotide compound is useful for preparing a composition for treating hyperproliferative disorder e.g. cancer. This sequence represents a human peroxisome proliferator-activated receptor-alpha (PPAR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence represents a PCR primer use to isolate DNA encoding the Shistosoma glutathion s-transferase protein. The amplified sequence can be used in a construct to transform the parasite of the invention. The parasite is a eukaryotic diploid multicellular parasite transformed with a transgene. Transgenic eukaryotic parasites are useful as universal grafts for in vivo delivery of beneficial gene product in humans and animals. The parasites can particularly be used for restoration of deficiencies whether acquired or genetic, such as hormone deficiencies, metabolic deficiencies, haematological deficiencies, immunological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryotic diploid multicellular parasite useful as universal grafts for invivo delivery of beneficial gene products in humans and animals involves transformation with a transgene.
receptor-alpha), that specifically hybridises with the nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GST-GPP fusion construct; circular; green fluorescent protein; glutathione S-transferase; eukaryotic diploid multicellular parasite; universal graft; transgenic eukaryotic parasite; acquired deficiency; genetic deficiency; hormone deficiency; metabolic deficiency; haematological deficiency; immunological deficiency; immunological deficiency; immunotherapy; anti-microbial therapy; anti-cancer therapy; drug addiction; poisoning condition; geriatric condition; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                           57.1%; Score 12; DB 12; Length 20; 100.0%; Pred. No. 2.9e+04; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                  Sequence 20 BP; 6 A; 4 C; 4 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                         -alpha) antisense oligonucleotide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 2; Page 36; 90pp; English.
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(first entry)
                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                              7 TATCTGAAGAGT 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 TATCTGAAGAGT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-412348/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PCR primer for GST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-DEC-1999;
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27-SEP-2000
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Thompson JD,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-AUG-1992;
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07-DEC-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-AUG-1992
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                                                                                                                                                                                                                                                                     AAQ51964;
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                                                                                                                                                                                                                         RESULT 31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention provides a method of diagnosing a vascular disease in an individual, involving determining the sequence at various polymorphic sites within the human thrombospondin 1 and thrombospondin 4 genes. The sequences at a number of polymorphic sites are also provided in the specification. In particular, the method can be used in the diagnosis of atherosclerosis, myocardial infarction, coronary heart
deficiencies, immunotherapy, anti-microbial therapy, anti-cancer therapy
                                                                                                                                                                                                                                                                                                                                    Human; variant thrombospondin 1; variant thrombospondin 4; SNP; polymorphism; vascular disease; coronary artery disease; forensics; myocardial infarction; atherosclerosis; stroke; venous thromboembolism; pulmonary embolism; paternity test; ds.
         They can also be used for treatment of drug addiction, of poisoning conditions, and for amelioration of geriatric conditions. Treatment of humans with in vivo transgenes are universally compatible, readily available and inexpensive. Genotypic alterations of the patients is avoided, reducing risks of mutagenesis and malignant transformation. (Updated on 06-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Daley GQ, Mccarthy JJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acids comprising single nucleotide polymorphisms, useful in applications such as forensics, paternity testing, medicine, genetic analysis and phenotype correlations to diseases such as diabetes and
                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag= a
/standard_name= "Single nucleotide polymorphism"
                                                                                                                                   ;
0
                                                                                                             Length 21;
                                                                                                                                  5; Indels
                                                                                       Sequence 21 BP; 4 A; 10 C; 3 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                 Human gene single nucleotide polymorphism #1912.
                                                                                                           Score 12; DB 3;
Pred. No. 3e+04;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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                                                                                                                                                        2 TGGCGTATCTGAAGAGTCTG 21
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                                                                                                            57.1%;
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2000US-0220947P.
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                                                                                                                                                                                                                                     AAF97151 standard; DNA; 21
                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                  (revised)
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                                                                                                                        Local Similarity
es 15; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
Unidentified
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26-JUL-2000;
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                                                                                                             Query Match
                                                                                                                                   Matches
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peripheral vascular diseases, venous thromboembolism and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Multiple drug resistance; mdr-1; ribozyme; membrane protein; liver; resistance; chemotherapeutic agent; colchicine; doxorubicin; colon; actinomycin D; vinblastine; small intestine; kidney; adrenal gland; adenocarcinoma; bowel; transformed phenotype; promyelocytic leukemia; human; chronic myelogenous leukemia; CML; follicular lymphocytic leukemia; breast cancer; colon carcinoma; neuroblastoma; lung cancer; genetic drift; mutation; hammerhead motif; hairpin; hepatitis delta virus; group I intron; RNaseP; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New enzymatic RNA molecules (ribozymes) - which cleave mRNA associated with tumours or mRNA expressed from gene encoding multiple drug
                           pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also useful in forensics, paternity testing, genetic analysis and phenotype correlations to diseases. The present sequence is an example of one of the human gene SNPS shown in the specification
                                                                                                                                                                                                                                                                                                                                                                             Gape
                                                                                                                                                                            was
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                                                                                                                                              _{\rm neviBeG} record issued on 18-NOV-2004 : The variantion feature incorrectly given a captial V
                                                                                                                                                                                                                                                                                                                       Length 21;
                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                    57.1%; Score 12; DB 4; Le
100.0%; Pred. No. 3e+04;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                          Sequence 21 BP; 5 A; S C; 6 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BCL-2 mRNA ribozyme cleavable nucleotide (2100).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      92US-00882885.
92US-00882885.
92US-00936421.
92US-00936422.
92US-00936531.
92US-00936531.
92US-00936531.
93US-00087131.
93US-00006122.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAQ51964 standard; RNA; 17 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93WO-US004573
                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.vv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                       10 CTGAAGAGTCTG 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Draper KG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTGAAGAGTCTG
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leukemia (CML), promyelocytic leukemia, Burkitt's lymphoma, or acute
lymphocytic leukemia, follicular lymphoma, B-cell acute lymphocytic
leukemia, breast cancer, colon carcinoma, neuroblastoma and lung cancer.
Cellular broteins which are able to control cellular proliferation and
are directly linked to a leukemic phenotype. These target sequences are
identified by the ribozyme of the invention. The ribozymes is formed in a
chammerhead motif, but may also be formed in the motif of a hairpin,
hepatitis delta virus, group I intron or RNaseP-like RNA. These ribozymes
corresponding gene. Cleavage of target mRNAs expression of a transformed
phenotype in man and other animals by modulating expression of the
corresponding gene. Cleavage of target mRNAs expressed in pre-neoplastic
and transformed cells elicits inhibition of the transformed state.
CMULtiple drug resistance water.) mRNA specific ribozymes remove the
cmechanism of drug resistance used by transformed cells and thus enhances
drug theraples for tumours. The ribozymes may also be used to study
corrected origins within cells. (Updated on 25-WAR-2003 to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes enzymatic nucleic acid molecules (NAMs) which specifically cleave RNA derived from an epidermal growth factor receptor (EGE-R) gene. AAV9721 to AAV96043 and AAV9999 to AAV99090 represent specifically claimed target sequence from human EGF-R. AAV98044 to AAV98866 and AAV98867 to V9878 represent hammerhead ribozymes and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Enzymatic nucleic acids - which cleave RNA derived from an epidermal growth factor receptor, useful for inhibiting cell proliferation and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human, epidermal growth factor receptor; EGFR; EGF-R; target sequence;
hammerhead ribozyme; hairpin ribozyme; inhibition; cell proliferation;
cancer; genetic drift; detection; mutation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                          Score 11.8; DB 2; Length 17;
Pred. No. 3.6e+04;
5; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human EGF-R target sequence nucleotide position 3856.
                                                                                                                                                                                                                                                                                                                                                          Sequence 17 BP; 3 A; 5 C; 3 G; 0 T; 6 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mcswiggen JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 5; Page 77; 109pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               667/c
AAV97667 standard; RNA; 17 BP.
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97US-00985162.
                                                                                                                                                                                                                                                                                                                                                                                              56.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 GTATCTGAAGAGTCT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 GUCUCUGAAGACUCU 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 53.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1998-437449/37
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                                                                                                                                                                                                                                                                                                                      correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              treating cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
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hairpin ribozymes respectively for human EGF-R. The NAMs are useful for cleaving EGF-R RNA in the treatment of a condition associated with EGFR expression levels e.g. to inhibit cell proliferation in the prevention or treatment of cancers. The NAMs can also be used as diagnostic tools to examine genetic drift and mutations within diseased cells or to detect the presence of EGF-R RNA in a cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic; cerebroprotective; nootropic; neuroprotective; antiparkinsonian; muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme; DNAzyme; incyyme; decleaver; amberzyme; inzyme; locygene; decleaver; amberzyme; linzyme; locygene; decleaver; almerzyme; lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia; human immunodeficiency virus; HTV associated NHL; mantle-cell lymphoma; MC1; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia; inflammatory arthropathy; central nervous system injury; cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis; chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS; parkinson's disease; ataxia; Huntington's disease; Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense constructs, which down regulate expression of a CD20 gene or neurite growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a nucleic acid molecule which down regulates expression of a CD20 gene and a nucleic acid molecule which down regulates expression of a neurite growth inhibitor gene (NOGO). The
                                                                                                                                                                                                  Gaps
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                                                                                                                                                             56.2%; Score 11.8; DB 2; Length 17; 86.7%; Pred. No. 3.6e+04; ive 0; Mismatches 2; Indels
                                                                                                                            Sequence 17 BP; 4 A; 5 C; 2 G; 0 T; 6 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chowrira BM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 30; Page 149; 200pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 central nervous system injury.
                                                                                                                                                                                                                                                                                                                                                              BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000US-0181797P
                                                                                                                                                                                                                                       7 TATCTGAAGAGTCTG 21
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                                                                                                                                                                                                                                                                                                                                                                ABK03278 standard; RNA; 17
                                                                                                                                                                                                                                                           TATCGAAAGAGTCTG 3
                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human CD20 Inozyme #229.
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CHOWRIRA B M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-607195/69.
                                                                                                                                                                                Local Similarity
hes 13; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                    12-MAR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                  ABK03278;
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(MCSW/)
(CHOW/)
                                                                                                                                                                     Query Match
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ABK03278/c
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Matches
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expression as indicator in diagnosis of tumour metastasis.
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CC DNAZYME) an Inozyme (an endolytic nucleic acids (e.g. a ribozyme or a DNAZYME) an Inozyme (an endolytic nucleic acid cleaving a an RNA molecule possessing an NCH motif), a G-cleaver (cleaving RNA with an NCH motif) prospecsing an NCH motif) proposessing an NCH motifi proposes of CD20 in the presence of a divalent cation that is preferably MG<sup>2</sup>+.

CC fCD20 in the presence of a divalent cation that is preferably MG<sup>2</sup>+.

CF but creat ment may further comprise the use of one or more conformation of CC CD2 of CD20 activity of the cell and treat a patient having a condition associated with the level conformation in particular, the CD20 targetting nucleic acid may be used to treat lymphoma (MCL), immunodeficiency virus) associated NHL, mantle-cell lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma, conforted acid is used to cleave RNA of the NGGO gene in the presence of a divalent cation that is preferably MG<sup>2</sup>+. Furthermore, the presence of a divalent cation that is preferably MG<sup>2</sup>+. Furthermore, the cucleic acid may be contacted with a cell to reduce NOGO activity of the coll and treat a patient having a condition associated with the level of therapies. In particular, the NOGO-targetting nucleic acid may be used to creat central nervous system (CNS) injury and cereboroscular accident (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS), chemotherapy-induced neuropathy, amyorrophic lateral acid may be used to create central nervous system (CNS) injury and cereboroscular accident connected neuropathy, amyorrophic lateral cation day disease, attack which respond to the modulation of NOGO expression. The present connected in the invention of characterial coll may be invention of the present coll and the invention of the inventio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human; cytokeratin; CK; LAMP; loop mediated isothermal amplification; tumour metastasis; prostate cancer; lymphoma; human; CK19; ss; primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LAMP nucleic acid amplification primers for detection of cytokeratin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           56.2%; Score 11.8; DB 4; Length 17; 86.7%; Pred. No. 3.6e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human cytokeratin 19-derived F3 PCR primer - SEQ ID 361.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 17 BP; 5 A; 6 C; 2 G; 0 T; 4 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence is an inozyme of the invention
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17-JUN-2002; 2002JP-00175271.
09-JUL-2002; 2002JP-00199759.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-MAY-2003; 2003WO-JP006256.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 GCGTATCTGAAGAGT 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16 GCGTATGTGCAGAGT 2
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Matches 13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Akai Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO2003097878-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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The invention relates to a novel method for selecting siRNA (short interfering RNA) comprising selecting an siRNA molecule of 19-25 mucleoside bases by selecting a target gene and measuring the functionality of sequences of 19-25 nucleotides in length that are substantially complementary to a stretch of nucleotides of the target sequence, where the functionality is dependent upon non-target specific criteria. Also claimed are methods for gene-silencing, developing an siRNA algorithm for selecting siRNA, selecting an siRNA with improved functionality, selecting bpy-functional siRNA, an siRNA molecule effective at silencing Bol-2, and a kit for gene silencing comprising the siRNA. The siRNA molecule comprises a sequence substantially similar to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                        The invention relates to novel nucleic acid amplification primers for the detection of human cytokeratin (CK) 18, 19 or 20 expression by the LAMP (loop mediated isothermal amplification) method. The primers of the invention may be useful for the detecting cytokeratin 18-20 expression as an indicator for the diagnosis of tumour metastasis, particularly prostate cancer and lymphoma. The amplification using the primers is highly efficient and allows very sensitive detection of tumour metastasis. The current sequence is that of the human CK19-related PCR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               siRNA; gene silencing; Bcl-2; optimised; short interfering RNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Anti-FLT1 siRNA related DNA sequence SEQ ID NO:736.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                56.2%; Score 11.8; DB 12;
86.7%; Pred. No. 3.6e+04;
ative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 17 BP; 4 A; 5 C; 5 G; 3 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 12; SEQ ID NO 736; 199pp; English.
Claim 19; SEQ ID NO 361; 266pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-NOV-2003; 2003WO-US036787.
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10-SEP-2003; 2003US-0502050P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CTGGCGTATCTGAAG 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTGGCCTACCTGAAG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADQ61034 standard; RNA; 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                         primer of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Anastasia K, Angela R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of the target sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
es 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RNA interference.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO2004045543-A2.
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sequence consisting of GGGAGAUAGUGAAGUA, GAAGUACAUCCAUUAUAAG, GUACGACAACCGGGAGAUA, AGAUACUGAUGUACU, UGAAGACUCUGCUCAGUUU, CAUGCGGCCUCUGUUUGA, UGCGGCCUCUGUUUGAUU, GAGAUAGUGAUGAUGAAGUACA, GGGGCCUCUGUUUGA, UGCGGCCUCUGUUUGAUU, AGAAGUAGUGAUGAAGUACA, GGGAGAUUGCUCAGUUUG. The sirNA molecule comprises a sense strand and an anti-sense strand. The sirNA molecule comprises a hairpin. The sirNA molecule comprises between 18 and 30 base pairs. The kit comprises at least two sirNA, comprising a first optimised sirNA and a second optimised sirNA. The method is useful in selecting sirNA and a second optimised sirNA. The method is useful in selecting used in the exemplification of the invention. The sequence is shown in the specification as DNA, but described as sirNA.
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                                                                                                                                                                                                                                                                                                                                                                                                       cytostatic, anticonnulsant, notropic, muscula, anti-HIV;

RNA interference, iRNA, antisense technology, lipid metabolism;

cholesterol imbalance, dyslipidemia hypercholesterolaemia;

coronary artery disease, CAD, coronary heart disease, CHD,

atherosclerosis, hepatic glucose production;

glucose-metabolism-related disorder, diabetes, cancer; breast cancer;

colon cancer; lung cancer; neurological disease, Huntington disease;

spinocerebellar ataxia, viral disease; AIDS; apolipoprotein B; apoB; ss.
                                                                                                                                                                                                                                                                                                                                                                                              vasotropic; antiarteriosclerotic; antidiabetic;
                                                                                                                                                                                             Gaps
                                                                                                                                                                                             o;
                                                                                                                                                                    56.2%; Score 11.8; DB 12; Length 19; 86.7%; Pred. No. 3.7e+04; ive 0; Mismatches 2; Indels (
                                                                                                                                                                                                                                                                                                                                                                        Human apolipoprotein B (ApoB) oligonucleotide segid 3822.
                                                                                                                                              Sequence 19 BP; 7 A; 2 C; 7 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2003US-0454265P.
2003US-0454962P.
2003US-0455050P.
                                                                                                                                                                                                                                                                                                    ADR79337 standard; DNA; 19 BP
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2003US-0493986P.
2003US-0494597P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14-APR-2003; 2003US-0452894P
17-APR-2003; 2003US-0463772P
25-APR-2003; 2003US-0465665P
25-ARR-2003; 2003US-0465802P
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2003US-0510246P.
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07-NOV-2003; 2003US-0518453P.
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                                                                                                                                                                                                                    3 GGCGTATCTGAAGAG 17
                                                                                                                                                                                                                                         GACGTAACTGAAGAG 16
                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                           13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bumcrot D;
                                                                                                                                                                                                                                                                                                                                                                                                 cardiant;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2004-677362/66.
                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO2004080406-A2.
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13-MAR-2003;
13-MAR-2003;
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08-AUG-2003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-AUG-2003;
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                                                                                                                                                                                                                                                                                                                           ADR79337;
                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                            RESULT 36
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      8888888888888888
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The invention describes a RNA interference (iRNA) agent (I) comprising a sense sequence and an antisense sequence, where the sense sequences have one or more asymmetrical phosphorothicate modifications comprising (C one or more asymmetrical phosphorothicate modifications and the antisense sequence targets a human gene sequence. Also described and the antisense sequence targets a human gene sequence. Also described comprising (I), involves selecting a sequence with activity and levals or glucose-6-phosphatase levels in a subject; producing (I); involves selecting a sequence with activity and cirroration decreases nuclease sensitivity while not decreasing its crivity; a kit comprising (I) and instruction for its use; and a device the modification decreases nuclease sensitivity while not decreasing its activity; a kit comprising (I) and instruction for its use; and a device that can be dispense or administer a composition comprising (I). (I) is useful for reducing apoB-100 levels or glucose-6-phosphatase levels. While the subject is suffering from a disorder characterised by elevated or cherwise unwanted expression of apoB-100, elevated or cherwise unwanted corporation of some of lipid metabolism. The characterised cholesterol, and/or disregulation of lipid metabolism. The hypercholesterolaemia, coronary artery disease (CAD), coronary heart of disparses (CAD) and atherosclerosis. (I) is administered to a subject to inhibit hepatic glucose production or for treating glucose-metabolism-crelated diseases as mentioned above, cancer (e.g. breast, colon or contracting the diseases as mentioned above, cancer (e.g., breast, colon or contracting the diseases as mentioned above, cancer (e.g., breast, colon or contracting the diseases as mentioned above, cancer (e.g., breast, colon or contraction B (AppB) antisense oligonucleotide that the medical control and the control and active and administrated and active and active and administrated and active and administrated and active and administrated and active and administrated 
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Interference RNA agent useful for treating dyslipidemias, coronary artery disease, diabetes, cancer or neurological disease, comprises sense sequence and antisense sequence which has specific modifications.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antilipemic; cardiant; vasotropic; antiarteriosclerotic; antidiabetic; cytostatic; anticonvulsant; nootropic; muscula; anti-HIV; MAX interference; iRNA; antisense technology; lipid metabolism; cholesterol imbalance; dyslipidaemia hypercholesterolaemia; coronary artery disease; CAD; coronary heart disease; CHD; atherosclerosis; hepatic glucose production; glucose-metabolism-related disorder; diabetes; cancer; breast cancer; colon cancer; lung cancer; neurological disease; Huntington disease; spinocerebellar ataxia; viral disease; AIDS; apolipoprotein B; apoB; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 19 BP; 5 A; 5 C; 4 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      can be used to control ApoB gene expression.
                                                                                                                                                                                                           Example 5; SEQ ID NO 3822; 378pp; English
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nes 13; Conservative
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Human apolipoprotein B (ApoB) oligonucleotide seqid 358.

(first entry)

16-DEC-2004

ADR75873;

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The invention describes a RNA interference (IRNA) agent (I) comprising a sense sequence and an antisense sequence, where the sense sequences have cone or more asymmetrical 2'-0 alkyl modifications, the antisense sequences to more asymmetrical phosphorothicate modifications and the antisense sequence targets a human gene sequence. Also described and the antisense sequence targets a human gene sequence. Also described care: a pharmaceutical preparation comprising (I); reducing (MI) apob-100 levels or glucose-6-phosphatase levels in a subject; producing (I); involves selecting a sequence with activity and introducing one or more asymmetrical modification in the sequence, where the modification decreases nuclease sensitivity while not decreasing its activity; a kit comprising (I) and instruction for its use; and a device that can be dispense or administer a composition comprising (I). Iis call is useful for reducing apoB-100 levels or glucose-6-phosphatase levels. Cotherwise unwanted expression of ago-100, elevated or cherwise unwanted corporation of lipid metabolism. The cherwise unwanted expression of ago-100, elevated or cherwise unwanted corporation of lipid metabolism. The disorder is chosen from the HDL/LDL cholesterol imbalance, coronary actory disease (CAD), coronary heart of disease (CAD) and atherosclerosis. (I) is administered to a subject to cinhibit hepatic glucose production or for treating glucose-metabolism. Cornation of diseases as mentioned above, cancer (e.g. breast, colon or corpus treating glucose-metabolism elements a human apolipoproclaim B (ApoB) antisense or glucose or general disease or complexed or control disease or control and sease as mentioned above, cancer (e.g., breast, colon or control proceed or control or cont
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Interference RNA agent useful for treating dyslipidemias, coronary artery disease, diabetes, cancer or neurological disease, comprises sense sequence and antisense sequence which has specific modifications.
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                                          12-MAR-2003; 2003US-0454265P.
13-MAR-2003; 2003US-0454562P.
13-MAR-2003; 2003US-0455650P.
14-APR-2003; 2003US-0462894P.
17-APR-2003; 2003US-0465772P.
25-APR-2003; 2003US-046565P.
                                                                                                                                                                                                                         09-MAY-2003; 2003US-0469612P.
08-AUG-2003; 2003US-0493986P.
11-AUG-2003; 2003US-0494597P.
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09-OCT-2003; 2003US-0510246P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Manoharan M, Bumcrot D;
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Gaps
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0
56.2%; Score 11.8; DB 13; Length 19; 86.7%; Pred. No. 3.7e+04; tive 0; Mismatches 2; Indels (
                    Best Local Similarity 86.7
Matches 13; Conservative
    Query Match
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ADR75873 standard; DNA; 19 BP. ADR75873/c ID ADR758 XX RESULT 38

dyslipidaemias, hypercholestorolaemia, statin-resistant hypercholesterolaemia, coronary artery disease (CAD), coronary heart disease (CHD) and atherosclerosis. (I) is administered to a subject to

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The invention describes a RNA interference (1RNA) agent (1) comprising a sense sequence and an antisense sequence, where the sense sequences have one or more asymmetrical 2.0 alkyl modifications, the antisense sequence targets a human gene sequence. The antisense and the antisense sequence targets a human gene sequence. Also described are a pharmaceutical preparation comprising (1); reducing (M1) apoB-100 levels or glucose-6-phosphatase levels in a subject; producing (M1) apoB-100 introducing one or more asymmetrical modification in the sequence, where the modification decreases nuclease sensitivity while not decreasing its activity; a kit comprising (1) and instruction for its use; and a device that can be dispense or administer a composition comprising (1). Is a custil for reducing apoB-100 levels or glucose-6-phosphatase levels. The subject is suffering from a disorder characterised by elevels.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              artery
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                                                                                            antilipemic; cardiant; vasotropic; antiarteriosclerotic; antidiabetic; cytostatic; anticonvulsant; nootropic; muscula; anti-HTV; why intiaense technology; lipid metabolism; cholesterol imbalance; dyslipidaemia hypercholesterolaemia; coronary artery disease; CAD; coronary heart disease; CHD; atherosclerosis; hepatic glucose production; glucose-metabolism-related disorder; diabetes; cancer; breast cancer; spinocere, lung cancer; neurological disease; Huntington disease; spinocerebellar ataxia; viral disease; AIDS; apolipoprotein B; apoB; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Interference RNA agent useful for treating dyslipidemias, coronary disease, diabetes, cancer or neurological disease, comprises sense sequence and antisense sequence which has specific modifications.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 5; SEQ ID NO 358; 378pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                      2003US-0454265P.
2003US-0454962P.
2003US-0465609P.
2003US-0463772P.
2003US-046565F.
2003US-0465665P.
2003US-0465665P.
2003US-0465802P.
2003US-0465802P.
2003US-0465802P.
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Example 5; SEQ ID NO 2187; 378pp; English.
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inhibit hepatic glucose production or for treating glucose-metabolism-related disorder e.g. diabetes or type-2 diabetes. (I) is useful for treating the diseases as mentioned above, cancer (e.g. breast, colon or lung cancer), neurological disease (e.g., Huntington disease or spinocerebellar ataxia) or viral disease (e.g., AlDS). This sequence represents a human apolipoprotein B (ApoB) antisense oligonucleotide that can be used to control ApoB gene expression.
                                                                                                                                                                                                                                                                                                                                   antilipemic; cardiant; vasotropic; antiarteriosclerotic; antidiabetic; cytostatic; anticonvulsant; nootropic; muscula; anti-HIV; kNA interference; iRNA; antisense technology; lipid metabolism; cholesterol imbalance; dyslipidaemia hypercholesterolaemia; coronary artery disease; CAD; coronary heart disease; CHD; atherosclerosis; hepatic glucose production; glucose-metabolism-related disorder; diabetes; cancer; breast cancer; colon cancer; lung cancer; neurological disease; Huntingcon disease; spinocerebellar ataxia; viral disease; AIDS; apolipoprotein B; apoB; ss.
                                                                                                                                         Gaps
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                                                                                                                 56.2%; Score 11.8; DB 13; Length 19; 86.7%; Pred. No. 3.7e+04; ive 0; Mismatches 2; Indels (
                                                                                                                                                                                                                                                                                                                Human apolipoprotein B (ApoB) oligonucleotide seqid 2187.
                                                                                           Seguence 19 BP; 5 A; 5 C; 4 G; 5 T; 0 U; 0 Other;
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2003US-0455050P.
2003US-0462894P.
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11-AUG-2003; 2003US-0494597P.
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les 13; Conservative
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14-APR-2003;
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Line invencion describes a knw interference (iktw) agent (1) comprising a sense sequence and an antisense sequence, where the sense sequences have one or more asymmetrical phosphorothicate modifications are sequences have one or more asymmetrical phosphorothicate modifications are and the antisense sequence targets a human gene sequence. Also described are: a pharmaceutical preparation comprising (1); reducing (MI) apoB-100 levels or glucose-6-phosphatase levels in a subject; producing (1); estabilising (1), involves selecting a sequence with activity and introducing one or more asymmetrical modification in the sequence, where the modification decreases nuclease sensitivity while not decreasing its critical modification for its uses and a device that can be dispense or administer a composition comprising (1). (1) is useful for reducing apoB-100 levels or glucose-6-phosphatase levels. CT he subject is suffering from a disorder characterised by elevated or otherwise unwanted expression of apoB-100, elevated or otherwise unwanted expression of apoB-100, elevated or otherwise unwanted compression of apoB-100, elevated or otherwise unwanted expression of apoB-100, elevated or otherwise unwanted compression of apoB-100, elevated or otherwise unwanted expression of apoB-100, clevated or otherwise unwanted compression of apoB-100, elevated or otherwise unwanted compression of apoB-100, clevated or otherwise unwanted expression of apoB-100, elevated or otherwise unwanted compression of apoB-100, clevated or otherwise unwanted compression of apoB-100, elevated or otherwise unwanted disorder e.g. disbetes or for treating glucose production or for treating glucose metabolism.

CC treating the diseases as mentioned above, cancer (e.g. breast, colon or creating the diseases as mentioned above, cancer (e.g. breast, colon or cupression), neurological disease (e.g., Muntington disease or cupression be used to control ApoR-cone elevated.
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invention describes a RNA interference (iRNA) agent (I)
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12-MAR-2003; 2003US-0454265P.
13-MAR-2003; 2003US-0454962P.
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connected the service of the service of the service of the services have concerned an antisense sequence. Where the sense sequences have one or more asymmetrical phosphorothicate modifications cand the antisense sequence targets a human gene sequence. Also described are: a pharmaceutical preparation comprising (1); reducing (M1) apo8-100 levels or glucose-6-phosphatase levels in a subject; producing (1); setabilising (1); involves selecting a sequence with activity and introducing one or more asymmetrical modification in the sequence, where the modification decreases nuclease sensitivity while not decreasing its cortivity; a kit comprising (1) and instruction for its use; and a device that can be dispense or administer a composition comprising (1). (1) is useful for reducing apo8-100 levels or glucose-6-phosphatase levels. (The subject is suffering from a disorder characterised by elevated or otherwise unwanted expression of apo8-100, elevated or otherwise unwanted expression of apo8-100, elevated or otherwise unwanted checkerolastor disregulation of lipid metabolism. The disparse (THD and othersecolastor), and/or disregulation of lipid metabolism. The chosenterolasmia, statin-resistant controlasmia, statin-resistant controlasmia, coronary artery disease (CAD), coronary heart of inhibit hepatic glucose production or for treating glucose-metabolism. Creating the diseases as mentioned above, cancer (e.g. breast, colon or inhibit hepatic glucose production or for treating glucose-metabolism. Creating the diseases as mentioned above, cancer (e.g. breast, colon or treating glucose-ballar ataxia) or viral disease (e.g., ADS). This sequence conserved the control of the control of
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                         14-APR-2003; 2003US-0462894P.
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25-APR-2003; 2003US-0465665P.
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09-MAY-2003; 2003US-0469612P.
08-AUG-2003; 2003US-0493986P.
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09-OCT-2003; 2003US-0510246P.
10-OCT-2003; 2003US-0510318P.
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2003US-0455050P
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US-09-001-826-16
US-09-091-952A-169
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US-09-629-644A-228
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US-08-849-488-12
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1916, Ap
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', App
                                                                                                                                                            August 12, 2005, 09:56:43 ; Search time 95 Seconds (without alignments) 361.703 Million cell updates/sec
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
                          GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-638-857-3
US-08-08-162-448
US-08-401-063-448
US-08-401-063-449
US-08-985-162-449
US-08-985-162-449
US-08-717-291-8
US-08-401-063-449
US-08-401-063-449
US-08-401-063-449
US-09-433-699-73
US-09-431-699-73
US-09-431-699-73
US-09-401-18
US-09-401-063-447
US-09-401-063-447
US-09-401-063-447
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US-09-401-063-447
US-09-108-452A-1366
US-09-108-452A-1366
US-09-280-805-129
US-09-118-452A-136
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Maximum Match 100%
Listing first 100 summaries
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Gapop 10.0 , Gapext 1.0
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Query
Match
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1398, Ap 9827, Ap 87, Appl 6, Appli

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Appl Appl App

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4507, Ap 33, Appl

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US-08-842-079-3
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                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 61.9%; Score 13; DB 3; Length 20; Best Local Similarity 100.0%; Pred. No. 2.9e+03; Matches 13; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61.9%; Score 13; DB 4; Length 20; 100.0%; Pred. No. 2.9e+03; tive 0; Mismatches 0; Indels
                                                                                                                      APPLICANT: BUELL, GARY N.
APPLICANT: BUELL, GARY N.
APPLICANT: SURPRENANT, ANNWARIE
APPLICANT: KAMASHIMA, BRIC
TITLE OF INVENTION: A PURINERGIC RECEPTOR
FILE REFERENCE: 1430-160
CURRENT APPLICATION NUMBER: US/08/842,079
CURRENT FILING DATE: 1997-04-28
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin Ver: 2.0
SOFTWARE: Patentin Ver: 2.0
SERGIP 20
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; Sequence 448, Application US/08985162
; Patent No. 6057156
                                                                             ; Sequence 3, Application US/08842079; Patent No. 6133434; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 13; Conserv
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US-09-638-857-3
                                                RESULT 1
US-08-842-079-3
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LENGTH: 20
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| Sequence 448, Application US/09401063 |
| Patent No. 6623962 |
| GENERAL INFORMATION: Achtar, Saghir |
| APPLICANT: Achtar, Saghir |
| APPLICANT: Achtar, Saghir |
| APPLICANT: Achtar, Saghir |
| TILLE OF INVENTION: ENZWAMIC NUCLEIC ACID TREATMENT |
| TITLE OF INVENTION: ENZWAMIC NUCLEIC ACID TREATMENT |
| TITLE OF INVENTION: TO LEVELS OF EPIDERMAL GROWTH |
| TITLE OF INVENTION: PACTOR RECEPTORS |
| NUMBER OF SEQUENCES: 1877 |
| CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSE: Lyon & Lyon |
| CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSE: Lyon & Lyon |
| Contraction |
| C
APPLICANT: ACKLAIR, Saghir
APPLICANT: Fell, Patricia
APPLICANT: Fell, Patricia
APPLICANT: Fell, Patricia
APPLICANT: Fell, Patricia
APPLICANT: McSwiggen, James APPLICANT: MCSwiggen, James APPLICANT: MCSwiggen, James APPLICANT: MCSWIGGEN, TO LEVELS OR CONDITIONS RELATED TITLE OF INVENTION: TO LEVELS OR ERPIDERMAL GROWTH
TITLE OF INVENTION: FACTOR RECEPTORS
NUMBER OF SEQUENCES: 1877
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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Best Local Similarity 87.5%; Pred. No. 3.6e+03;
Matches 14; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,162
PILING DATE: 04 December 1997
CLASSIFICATION 1514
PRIOR APPLICATION NUMBER: 60/036,476
FILING DATE: 31 January 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 230/107
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633 West Fifth Street
Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 230/
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      448:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
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CITY: Los Angeles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-985-162-448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 134, Application US/07982759F
Facent No. 6057123
GENERAL INFORMATION:
APPLICANT: CRAIG, Stewart
APPLICANT: GEORGE, Michael
APPLICANT: GEORGE, Michael
APPLICANT: CARPLEWSKI, Lloyd George
APPLICANT: GILBERT Richard
TITLE OF INVENTION: Stem Cell Inhibiting Proteins
NUMBER OF SEQUENCES: 178
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: TEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/982,759F
PILING DATE: 08-MAR-1993
PRIOR APPLICATION NUMBER: US/07/982,759F
FILING DATE: 23-DEC-1991
PRIOR APPLICATION NUMBER: GB 9127319.3
ATTORNEY/AGENT INFORMATION:
NAME: BAKER, HOLLIE L.
REGISTRATION NUMBER: 31,321
REGISTRATION NUMBER: 31,321
REGISTRATION NUMBER: 31,321
REGISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAX: 617-526-6000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature
LOCATION: 1..20
OTHER INFORMATION: /product= "BB9513 oligomer"
FILING DATE: 14-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: BAKEN: HOLLIE L.
REGISTRATION NUMBER: 11,321
REFERENCE/DOCKET NUMBER: 102.378.120DV-2
TELEPHONE: 617-526-6110
TELEPHONE: 617-526-6000
INFORMATION FOR SEQ ID NO: 134:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
TYPE: NUCleic acid
STRANDENNES: single
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STREET: 60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 617-526-5000
INFORMATION FOR SEQ ID NO: 134:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17 CTGACGCATCTGAAGA 2
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Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: DNA
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STREET: bo
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TYPLICAN:
NUMBER OF SEQUENCES: 178
CORRESPONDENCES. 178
CORRESPONDENCE ADDRESS:
ADDRESSEE: HALE and DORR
STREET: 60 State Street
CITY: Boston
STATE: MA
ZIP: 02109
COMPUTER READBALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN DATA:
APPLICATION NUMBER: US/08/450,905B
FILING DATE: 26-MAR-1995
FILING DATE: 08-MAR-1995
FILING DATE: 08-MAR-1993
FRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9127319.3
FRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9221587.0
                                                                                                                                                                                                                                                                                                                                       APPLICATION.
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/985,162
FILING DATE: 04 December 1997
APPLICATION NUMBER: 60/036,476
FILING DATE: 13 January 1997
ATTORNEY AGENT INFORMATION:
NAME: WAIDLEY RICHARD 3.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 32,327
RELEPAN: (213) 489-1600
TELEPAN: (213) 955-0440
TE
                                        COUNTRY: U.S.A.

ZIP: 90071-206

ZIP: 90071-206

ZIP: 90071-206

ZOMPUTER READBLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

MEDIUM TYPE: 450.789

COMPUTER: 1BM Compatible

OPERATING SYSTEM: 1BM P.C. DOS 5.0

SOFTWARE: FRAISEQ for Windows 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/401,063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-450-905B-134/c
; Sequence 134, Application US/08450905B
; Patent No. 5856301
; GENERAL INFORMATION:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 GTATCTGAAGAGTCTG 21
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Best Local Similarity 87.5
Matches 14; Conservative
                California
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US-09-401-063-448
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17 GGGTATCGAAAGAGTCT 1
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STATE: California
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Sequence 449, Application US/08985162

APPLICANT: McSwiggen, James

TITLE OF INVENTION: ENTYMATIC NUCLEIC ACID TREATMENT

TITLE OF INVENTION: TACTOR RECEPTORS

NUMBER OF SEQUENCES: 1877

CORRESPONDENCE ADDRESS: 1877

CORRESPONDENCE ADDRESS: 1877

CORRESPONDENCE NUMBER: 1870

STREET: Suite 4700

CITY: LOS Angels

STREET: US.A.

ZIP: 90071-2066

CONPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

MEDIUM TYPE: 3.5" Diskette, 1.97

CORRENT APPLICATION DATA:

APPLICATION NUMBER: 60/036,476

FILING DATE: 31 January 1997

ATTOMENEY/AGENT INFORMATION:

NAME: Warburg, RACHARG J.

RESERRANCE (213) 489-1600

TELEFONMUTION NUMBER: 3.30/107

TELECOMMUNICATION NUMBER: 3.30/107

TELEFONMUTION FOR SEQ ID NO: 449:

SEQUENCE (213) 489-160

TELEFONMUTION FOR SEG ID NO: 449:

SEQUENCE (213) 489-160

TELEFONG: (213) 480-160

TELEFONG: (213) 4
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                                                                                                                                                                                                                                                                                  61.0%; Score 12.8; DB 3; Length 20;
87.5%; Pred. No. 3.6e+03;
tive 0; Mismatches 2; Indels
                                                                                                                  NAME/KEY: misc_feature
LOCATION: 1..20
CTHER INFORMATION: /product= "BB9513 oligomer"
US-07-982-759F-134
                                                                                                                                                                                                                                                                                                                                                                                                               1 CTGGCGTATCTGAAGA 16
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Best Local Similarity 82.4'
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                               Best Local Similarity 87.5
Matches 14; Conservative
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STRANDEDNESS: single
STRANDEDNESS: single
TOPOLOGY: linear
                                   TOPOLOGY: linear MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
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4 GCGTATCTGAAGAGTCT 20

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| Sequence 4.01 - 053 - 445/C
| Sequence 4.02 - 403 - 403/C
| Patent No. 6621928
| Patent No. 6621928
| Patent No. 66219204
| Sequence 4.02 - 403/C
| Patent No. 66219204
| Pate
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REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                       14; Conservative
                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: sing
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Best Local Similarity
Matches 14; Conserv
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US-09-371-772B-5737
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| Sequence 8, Application US/08728603
| Patent No. 6093806
| GENERAL INFORMATION:
| APPLICANT: Cesarman, Ethel APPLICANT: Knowles, Daniel M.
| TITLE OF INVENTION: PROTEINS OF KAPOSI'S SARCOMA ASSOCIATED ITLE OF INVENTION: PROTEINS OF KAPOSI'S SARCOMA ASSOCIATED CORRESPONDENCE ADDRESS:
| ADDRESSEE: NIXON HARGRAVE, DEVANS & DOYLE LLP STREET Clinton Square, P.O. Box 1051
| CITY: Rochester STATE: New York COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ch 58.1%; Score 12.2; DB 2; Length 20; al Similarity 82.4%; Pred. No. 7.3e+03; 14; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/728,603
FILING DATE: 10-OCT-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BRANAN, SUSAN J.
REGISTRATION NUMBER: 34,103
                                                                                                                                                                                                         COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: RAOPY disk

COMPUTER: BAP PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURSIT APPLICATION DATA:

APPLICATION NUMBER: US/08/717,291

FILING DATE:

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: BRAMAN, SUSAN J.

REFERENCE/DOCKET NUMBER: 19603/1360

TELEPOOMMICATION INFORMATION:

TELECOMMICATION INFORMATION:

TELECOMMICATION INFORMATION:

TELEPHONE: 716-263-1636
APPLICANT: Mesri, Enrique
TITLE OF INVENTION: KSHV POSITIVE CELL LINES
NUMBER OF SEQUENCES:
ORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON, HARGRAVE, DEVANS & DOYLE LLP
STREET: Clinton Square, P.O. Box 1051
CITY: Rochester
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 CGTATCTGAAGAGTCTG 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-717-291-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS: LENGTH: 20 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           716-263-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Bavco, Pam
APPLICANT: Bavco, Pam
APPLICANT: Stinchcomb, Dan
APPLICANT: McSudgen, Jaime
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
TITLE OF INVENTION: Manber: US/09/371,772B
CURRENT FILING DATE: 1999-08-10
PRIOR FILING DATE: 1995-10-26
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US-09-433-699-73/C

Sequence 73, Application US/09433699B

Patent No. 6165786

GENERAL INFORMATION:

APPLICANT: C. Frank Bennett

APPLICANT: Lox M. Cowsert

TITLE OF INVENTION: ANTISENSE MODULATION OF NUCLEOLIN EXPRESSION

FILE REFERENCE: RTS-0109

CURRENT APPLICATION NUMBER: US/09/433,699B

CURRENT FILING DATE: 1999-11-03

NUMBER OF SEQ ID NOS: 89

SEQ ID NO 73

LENGTH: 20
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75.0%; Pred. No. 9.3e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
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19603/720
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Patent No. 6566127
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                   TELECOMMUNICATION INFORMATION:
TELEPHONE: 716-263-1636
TELEPAX: 716-263-1600
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20 receasicrasaecinic
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                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 CGTATCTGAAGAGTCTG 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 14225
SOFTWARE: Patentin version 3.0
SEQ ID NO 5737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Artificial Sequence
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Matches 15, Conservative
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GENERAL INFORMATION:
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90017
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                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-461-503-4
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                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/07852260
Fatent No. 5525715
GENERAL INFORMATION:
APPLICANT: Recaniello, Vincent
APPLICANT: Tatem, Joanne M.
TITLE OF INVENTION: METHODS FOR PRODUCING RNA VIRUSES FROM
TITLE OF INVENTION: aDNA
NUMBER OF SEQUENCES: 9
CORRESPONDENCE 3.9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Gooper & Dunham
STREET: 30 Rockefeller Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                          Score 11.8; DB 4; Length 16;
Pred. No. 1.1e+04;
                                                                                                                                                                                                                           2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 30 RUCLARY
CITY: New YORK
STATE: New YORK
COUNTRY: U.S.A.
ZIP: 10112
ZP: 10112
COMPUTER HEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN POTA:
APPLICATION DATA:
APPLICATION NUMBER: US/07/852,260
FILING DATE: 19920619
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 36,07-B-PCT-US
TELEPRAY: (212) 977-9550
TELEFAX: (212) 644-0525
TELEFAX: (212) 644-0525
TELEFAX: (212) 647-0525
                                                                                                                                                                                                                           2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 18, Application US/07936421
; Patent No. 5750390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                          56.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 GGCGTATCTGAAGAG 17
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                                                                                                                                                                                                                                                                                                                              GACGUAACUGAAGAG 16
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                                                                                                                                                                                                                           11; Conservative
                                TYPE: RNA
ORGANISM: Homo sapiens
                                                                                                                                                          Query Match
Best Local Similarity
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Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HYPOTHETICAL: N
HYPOTHETICAL: NO
HYPOTHETICAL: NO
HYPOTHETICAL: NO
HYPOTHETICAL: NO
US-07-852-260-4
                                                                                               US-09-371-772B-5737
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US-07-936-421-18
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US-07-852-260-4
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                                                                                                                                                                                                                               Matches
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Gaps
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; Sequence 4, Application US/08461503
; Patent No. 5834302
; GENERAL INFORMATION:
APPLICANT: Tatem, Joanne M.
APPLICANT: Weeks-Levy, Carclyn L.
APPLICANT: Weeks-Levy, Carclyn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
APPLICANT: James D. Thompson
APPLICANT: Kenneth G. Draper
TITLE OF INVENTION: METHOD AND REAGENT FOR
TITLE OF INVENTION: TREATMENT OF DISEASES CAUSED
TITLE OF INVENTION: BY EXPRESSION OF THE BCL-2
TITLE OF INVENTION: GENE
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSE: Lyon & Lyon
STREET: 611 West Sixth Street
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPOTER: 15M COMPARIZED:
COMPOTER: 15M COMPARIZED:
SOFTWARE: WordPerfect (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/936,421
FILING DATE: 19920826
CLASSIFICATION 435
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 197/243
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: 1BM Compatible
OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (213) 489-1600
(213) 955-0440
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
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Gaps
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APPLICANT: Racaniello, Vincent
APPLICANT: Tatem, Joanne M.
APPLICANT: Tatem, Joanne M.
APPLICANT: Tatem, Joanne M.
TITLE OF INVENTION: METHODS FOR PRODUCING RNA VIRUSES FROM
TITLE OF INVENTION: CDNA
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS
CORRESPONDENCE ADDRESS
CORRESPONDENCE ADDRESS
CORRESPONDENCE ADDRESS
COUNTY: US.A
ZIP: New York
COUNTY: US.A
ZIP: 10036
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release 1.30
CURRENT APPLICATION NUMBER: US/08/465,250
FILING DATE: 6-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 38,677
REFERENCE/DOCKET NUMBER: 38,678
REFERENCE/DOCKET NUMBER: 38,678
TELECOMMUNICATION INFORMATION:
TELECHOME: (212) 391-0525
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/08465250
Patent No. 6136570
                       TELECOMMUNICATION INFORMATION
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 GGCGTATCTGAAGAG 17
                                                                                                                                                                                                                                                                                                                                                                                                7 TATCTGAAGAGTCTG 21
                                                                                            TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
       REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                       17 TATCGAAGAGTCTG 3
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LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Matches 13; Conservative
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US-08-985-162-447
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US-08-465-250-4
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US-08-465-250-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 447, Application US/08985162
Patent No. 6057156
GENERAL INFORMATION:
APPLICANT: Akhtar, Saghir
APPLICANT: Fell, Patricia
APPLICANT: McSwiggen, James
TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT
TITLE OF INVENTION: OF DISEASES OR CONDITIONS RELATED
TITLE OF INVENTION: TO LEVELS OF EPIDERMAL GROWTH
TITLE OF INVENTION: FACTOR RECEPPORS
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,503
FILING DATE: 5-UN-1995
CLASSIPICATION: 435
ATTONNEY/AGENT INPORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REGISTRATION NUMBER: 28,678
REGISTRATION NUMBER: 278-0400
TELEFAX: (212) 278-0400
TELEFAX: (212) 278-0400
TELEFAX: (212) 278-0400
TELEFAX: (212) 391-0525
TELEX: 422523 COOP UI
SEQUENCE CHARATTERISTICS:
LENGTH: 17 base pairs
TYPE: mucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 11.8; DB 2;
Pred. No. 1.1e+04;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: STORAGE
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FASTESO for Windows 2.0
CURRENT APPLICATION DATA:
RILING DATE: 04 December 1997
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
FILING DATE: 31 January 1997
ATYORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 1877
CORRESPONDENCE ADDRESS:
ADDRESSE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Warburg, Richard J. REGISTRATION NUMBER: 32,327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   56.2%;
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Best Local Similarity 86.7
Matches 13; Conservative
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HYPOTHETICAL: N
HATI-SENSE: NO
US-08-461-503-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-985-162-447/c
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Sequence 1366, Application US/09198452A
Fatent No. 6559294
GENERAL INFORMATION:
APPLICANT: Griffalas, R.
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prever TITLE OF INVENTION: and treatment of infection
TITLE REFERENCE: 9710-003-999
CURRENT APPLICATION NUMBER: US/09/198,452A
CURRENT FILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 6849
SEQ ID NO 1366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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Patent No. 625510
GENERAL INFORMATION:
APPLICANT: Jacqueline Wyatt
TITLE OF INVENTION:
ANTISENSE MODULATION OF ARA70 EXPRESSION
TITLE OF INVENTION:
ANTISE OF INVENTION:
ANTISENSE MODULATION OF ARA70 EXPRESSION
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/488,857B
CURRENT APPLICATION NUMBER: US/09/121
SEQ ID NOS:
SEQ ID NOS:
SEQ ID NOS:
LENGTH: 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 56.2%; Score 11.8; DB 3; Length 20; Best Local Similarity 86.7%; Pred. No. 1.2e+04; Matches 13; Conservative 0; Mismatches 2; Indels
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                        APPLICATION NUMBER: 60/036,476
FILING DATE: 31 January 1997
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET WINBER: 230/107
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION FOR 89-1600
TELERAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 447:
SEQUENCE CHARACTERISTICS:
   04 December 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17 TATCGAAAGAGTCTG 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGIH: 17 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TOPOLOGY: linear
US-09-401-063-447
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 20
US-09-488-857B-38/c
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                                                                                                                                                                                     Sequence 4438, Application US/09371772B

Sequence 4438, Application US/09371772B

Sequence 4438, Application US/09371772B

SERIER NOTE OF SEGERAL

APPLICANT: Pavco, Pam

APPLICANT: Pavco, Pam

APPLICANT: Stinchomb, Dan

APPLICANT: Escobedo, Jaime

TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re

TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor

TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor

TITLE OF INVENTION NUMBER: US/09/371,772B

CURRENT APPLICATION NUMBER: US 60/005,974

PRIOR FILING DATE: 1995-10-26

PRIOR FILING DATE: 1995-01-06

NUMBER OF SEQ ID NOS: 14225

SOFTWARE: PATCHELING CONTAINED NOT SECOLUMBER OF SEQ ID NOS: 14225

SOFTWARE: PATCHELING OF SECOLUMBER OF SEQ ID NOS: 14225
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 447, Application US/09401063
; Sequence 447, Application US/09401063
; Patent No. 6623962;
; GENERAL INFORMATION:
    APPLICANT: Pall, Patricia
    APPLICANT: Pall, Patricia
    APPLICANT: Pall, Patricia
    APPLICANT: PALL, Patricia
    APPLICANT: PALL, PARTICIA
    TITLE OF INVENTION: DO DISEASES OR CONDITIONS RELATED
    TITLE OF INVENTION: TO LEVELS OF EPIDERMAL GROWTH
    TITLE OF INVENTION: TO LEVELS OF EPIDERMAL GROWTH
    TITLE OF INVENTION: TO LEVELS OF EPIDERMAL GROWTH
    TITLE OF INVENTION: TO LEVELS OF EPIDERMAL
    TITLE OF INVENTION: TO LEVELS
    TITLE OF INVENTION: TO
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OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ for Windows 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/09/401,063
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/985,162
GGCGTATCTGACAAG 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 GGCGTATCTGAAGAG 17
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Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: RNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-401-063-447/C
                                                                                                                                              RESULT 18
US-09-371-772B-4438
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US-09-517-467B-30
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                                                                                                                                                                                                                                                                                                                                                               | FARENAL INFORMATION:
| GENERAL INFORMATION:
| APPLICANT: Barany, Francis
| APPLICANT: Liu, Janathao
| APPLICANT: Liu, Janathao
| APPLICANT: Liu, Janathao
| APPLICANT: Liu, Monib
| APPLICANT: Zirvi, Monib
| APPLICANT: Gerry, No. 6534293man P.
| APPLICANT: Gerry, No. 6534293man P.
| APPLICANT: Gerry, Philip P.
| TITLE OF INVENTION: POLYMORPHISMS AND ALIGNMENT OF CLONES IN GENOMIC
| TITLE OF INVENTION: SEQUENCING
| TITLE REFERENCE: 19603/2621
| CURRENT FILING DATE: 2000-01-05
| PRIOR APPLICATION NUMBER: 60/114,881
| PRIOR FILING DATE: 1999-01-06
| NUMBER OF SEQ ID NOS: 181
| SEQ ID NO 118
| LENGTH: 21
                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Description of Artificial Sequence: probe/primer
US-09-478-189-118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 56.2%; Score 11.8; DB 4; Length 21; 86.7%; Pred. No. 1.2e+04; tive 0; Mismatches 2; Indels
                                                                      Score 11.8; DB 4; Length 20;
Pred. No. 1.2e+04;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Loren J. Miraglia, Pamela Nero, Mark J.
APPLICANT: Graham, Brett P. Monia
TITLE OF INVENTION: ANTISENSE MODULATION OF HUMAN MDM2
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 271
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
IBM PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDERSKEE: Law Offices of Jane Massey Licata STREET: 66 East Main Street CITY: Marlton STRIE: W COUNTRY: U.S.A. ZIP: 08053
ZIP: 08053
ZOMPITER REALDABLE FORM: MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 129, Application US/09280805
Patent No. 6184212
                                                                                                                                                                                                                                                                                                                          Sequence 118, Application US/09478189
Patent No. 6534293
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OPERATING SYSTEM: WINDOWS 95
OCCUMARRE: WORDPERFECT 6.0
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-1366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Artificial Sequence
                                                                      56.2%;
86.7%;
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Best Local Similarity 86.7.
Then 13; Conservative
                                                                   Query Match 56.23
Best Local Similarity 86.77
Matches 13, Conservative
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US-09-280-805-129
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US-09-198-452A-2767/c

Sequence 2767, Application US/09198452A

Sequence 2767, Application US/09198452A

Sequence 2767, Application US/09198452A

GENERAL INFORMATION:

APPLICANT: Griffals, R.

TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragmente

TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, preve

TITLE OF INVENTION: and treatment of infection

FILE REPERBUCE: 9710-003-999

CURRENT APPLICATION NUMBER: US/09/198,452A
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Sequence 30, Application US/09517467B

Batent No. 6451602

GENERAL INFORMATION:

APPLICANT: Ian Popoff

APPLICANT: Lax M. Cowsert

TITLE OF INVENTION: ANTISENSE MODULATION OF PARP EXPRESSION

FILE REFERENCE: RTS-0150

CURRENT APPLICATION NUMBER: US/09/517,467B

PRIOR APPLICATION NUMBER: 09/517,467

PRIOR FILING DATE: 2000-03-02

PRIOR FILING DATE: 2000-03-02

NUMBER OF SEQ ID NOS: 345

SEQ ID NO 30

LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 11.6; DB 3;
Pred. No. 1.5e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Antisense Oligonucleotide US-09-517-467B-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                          NAME: Licata, Jane Massey
REGISTRATION NUMBER: 32,257
REGISTRATION NUMBER: ISPH-0346
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-810-1515
TELEPAX: 609-810-1454
UMBER: US/09/280,805
herewith
          APPLICATION NUMBER: US/09/280,80:
FILING DATE: herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/048,810
FILING DATE: MARCH 26, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Licata, Jane Massey
                                                                                                                                                                                                                                                                                                                   TELEPAX: 609-810-1454

INFORMATION FOR SEQ ID NO: 129:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
JANTI-SENSE: Yes
US-09-280-805-129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GCTTATCCGAGGCTCCG 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 77.8%;
Matches 14; Conservative
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ZIP: 48334
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54.3%;
                                                                                 Query Match 55.2%;
Best Local Similarity 91.7%;
Matches 11; Conservative
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Best Local Similarity 92.3
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTGGCTTATCTGA 5
                                                                                                                                                                       10 CTGAAGAGTCTG 21
                                                                                                                                                                                                ; ORGANISM: Homo sapiens
US-09-657-472-1916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo Sapiens
FEATURE:
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US-09-657-289A-12/C
; Sequence 12, Application US/09657289A
; Patent No. 6737245
; GENERAL INFORMATION:
; APPLICANT: Francis, Kevin P.
; APPLICANT: Contag, Pamela R.
; APPLICANT: Joh, Danny J.
; TITLE OF INVENTION: LUCIFERASE EXPRESSION CASSETTES AND METHODS OF USE
; TITLE OF INVENTION INCIPERASE EXPRESSION CASSETTES AND METHODS OF USE
; FILE REPERENCE: 9400-0006
; CURRENT APPLICATION NUMBER: US/09/657,289A
; CURRENT FILING DATE: 2000-09-07
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 12
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JAPPILCANT: Cargill, Michele

JAPPILCANT: Cargill, Michele

JAPPILCANT: Cargill, Michele

JAPPILCANT: Eladad, James S.

APPILCANT: Bolk, Stacey

APPILCANT: Bolk, Stacey

APPILCANT: Bolk, Stacey

APPILCANT: MCGARTHY, Jeanette J.

CURRENT MCGARTHY, Jeanette J.

TITLE OF INVENTION: SINGLE NUCLEOTIDE POLYMORPHISMS IN GENES

FILE REFERENCE: 2825.1027-001

CURRENT FAPLICATION NUMBER: US/09/657,472

PRIOR APPLICATION NUMBER: US 60/153,357

PRIOR APPLICATION NUMBER: US 60/220,947

PRIOR PILING DATE: 2000-09-06

PRIOR FILING DATE: 2000-07-26

PRIOR FILING DATE: 2000-08-16

NUMBER OF SEQ ID NOS: 2551

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Description of Artificial Sequence: LUXA-REV
US-09-657-289A-12
                                                                                                                                                                       Score 11.6; DB 4; Length 20;
Pred. No. 1.5e+04;
0; Mismatches 4; Indels
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Sequence 1916, Application US/09657472;

Patent No. 6727063;

GENERAL INFORMATION:
CURRENT FILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 6849
SEQ ID NO 2767
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 GCGTATCTGAAGAGTCTG 21
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                                                                                                                                                                                                                                                                                           20 GCTTCTCTGAACAGACTG 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19 GCATCTCTGAGGAGTGTG 2
                                                                                      ; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-2767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                     ch 55.2%;
il Similarity 77.8%;
14; Conservative
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Best Local Similarity
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Sequence 6466, Application US/09422978

Sequence 6466, Application US/09422978

Batent No. 6537751

GENERAL INFORMATION:
APPLICANT: Cohen, Daniel
APPLICANT: Cohen, Daniel
APPLICANT: Chumakov, Ilya
ITILE OF INVENTION: Biallelic markers for use in constructing a high density...
ITILE REFERENCE: GENSET. 020CP1
CURRENT FILING DATE: 1999-10-20
EARLIER APPLICATION NUMBER: US 09/298,850
EARLIER APPLICATION NUMBER: US 60/109,732
EARLIER PILING DATE: 1999-11-23
EARLIER PILING DATE: 1998-11-23
EARLIER FILING DATE: 1998-11-23
MUMBER: US 60/082,614
EARLIER FILING DATE: 1998-04-21
NUMBER: US 60/082,614
EARLIER FILING DATE: 1998-04-21
SARLIER PILING DATE: 1998-04-21
SARLIER POPULCATION NUMBER: US 60/082,614
EARLIER FILING DATE: 1998-04-21
SARLIER POPULCATION NUMBER: US 60/082,614
EARLIER FILING DATE: 1998-04-21
SARLIER POPULCATION NUMBER: US 60/082,614
EARLIER FILING DATE: 1998-04-21
SARLIER POPULCATION NUMBER: US 60/082,614
EARLIER FILING DATE: 1998-04-21
SARLIER POPULCATION NUMBER: US 60/082,614
EARLIER FILING DATE: 1998-04-21
SARLIER POPULCATION NUMBER: US 60/082,614
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OTHER INFORMATION: upstream amplification primer 99-11786 for SEQ 2552,
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Score 11.6; DB 4; Length 21;
Pred. No. 1.5e+04;
1; Mismatches 0; Indels
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Pred. No. 1.9e+04;
0; Mismatches 1; Indels
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US-08-602-093-12/c

Sequence 12. Application US/08602093

Patent No. 5837535

GENERAL INFORMATION:

APPLICANT: JOSEPH, Rajiv

APPLICANT: Ocoup, Dexian

TITLE OF INVENTION:

NUMBER OF SEQUENCES:

ADDRESSEE: Kohn & Associates

STREET: 30500 No. 5837535thwestern Hwy.

CITY: Farmington Hills

STATE: Michigan

COUNTRY: US
      6; bb
1.5e+04;
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                                                                                                    Query Match 53.3%; Score 11.2; DB 3; Length 17; Best Local Similarity 81.2%; Pred. No. 2.3e+04; Matches 13; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53.3%; Score 11.2; DB 4; Length 17; 81.2%; Pred. No. 2.3e+04; tive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MD
MEDIUM TYPE: storage
COMPUTER: IEM Compatible
OPERATING SYSTEM: IEM P.C. DOS 5.0
SOFTWARES: ReatSEQ for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/401,063.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/985,162
FILING DATE: 04 December 1997
APPLICATION NUMBER: 60/035,476
FILING DATE: 31 January 1997
ATTORNEY/AGBNT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REGISTRATION NUMBER: 32,327
RELEPHONE: (213) 489-1600
TELEPHONE: (213) 489-1600
TELEFAX: (213) 489-1600
                                                                                                                                                                                               4 GCGTATCTGAAGAGTC 19
                                                                                                                                                                                                                                       16 GGGTATCGAAAGAGTC 1
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Best Local Similarity 81.2'
Est Local 31 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
  ; TYPE: nucleic acid
; STRANDEDNESS: singl
; TOPOLOGY: linear
US-08-985-162-450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 90071-2066
                                                                                                                                                                                                                                                                                                                              US-09-401-063-450/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-401-063-450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: CE
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ð
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Pred. No. 1.9e+04;
0; Mismatches 1; Indels
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Patent No. 6057156
GENERAL INFORMATION:
APPLICANT: Akhtar, Saghir
APPLICANT: McSwiggen, James
TITLE OF INVENTION: BLAYMATIC NUCLEIC ACID TREATMENT
TITLE OF INVENTION: TO LEVELS OF EPIDERMAL GROWTH
TITLE OF INVENTION: TO LEVELS OF EPIDERMAL GROWTH
TITLE OF INVENTION: FACTOR RECEPTORS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/602,093
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kohn, Kenneth I.
REGISTRATION NUMBER: 30,995
REFERENCE/DOCKET NUMBER: 1059.00015
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1059-5055
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: STRANDENESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Los Angeles
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 1.5" Diskette, 1.44 Mb
MEDIUM TYPE: 1.5" DISKETTE, 1.00 S.0
SOFTWARE: FRACESO for Windows 2.0
CURRENT APPLICATION DATA: W10895,162
FILING DATE: 04 December 1997
CLASSIFICATION: 514
PRIGN APPLICATION: PIPPRAMATION:
ANDERSON WINDER: 00/036,476
FILING DATE: 31 January 1997
ATTORNEY APPLICATION: Piphard INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET UNMBER: 230/107
TELECOMMUNICATION: INFORMATION:
TELEPHONE: (213) 489-1600
TELERA: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 450:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 1877
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 613 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                     54.3%;
                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 92.3
Matches 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                  , TOPOLOGY: linear
US-08-602-093-12
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ORGANISM: Homo Sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-696-791-466/c
                                                                                                                                                                                                                                                                                            US-08-555-678-57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
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                                                                               APPLICANT: Cohen, Daniel
APPLICANT: Cohen, Daniel
APPLICANT: Chumenfeld, Marta
APPLICANT: Chumenfeld, Marta
APPLICANT: Chumenkevv, 11ya
TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
FILE REFERENCE: GENSET.020CP1
CURRENT APPLICATION NUMBER: US/09/422,978
CURRENT FILING DATE: 1999-04-21
EARLIER APPLICATION NUMBER: US 60/109,732
EARLIER FILING DATE: 1998-11-23
EARLIER FILING DATE: 1998-11-23
EARLIER FILING DATE: 1998-04-21
NUMBER OF SEQ ID NOS: 11796
SEQ ID NOS: 11796
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: primer_bind
LOCATION: 1..18
OTHER INFORMATION: upstream amplification primer 99-6097 for SEQ 1748,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53.3%; Score 11.2; DB 4; Length 18; 81.2%; Pred. No. 2.3e+04; tive 0; Mismatches 3; Indels
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Patent No. 5763174

GENERAL INFORMATION:
APPLICANT: Nishikura, Kazuko
ITILE OF INVENTION:
ITILE OF INVENTION: of Use Thereof
NUMBER OF SEQUENCES: 67

CORRESPONDENE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Cntr, P.O. Box 457

CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 19477

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/555,678
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/197,794
FILING DATE: 17-FEB-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/280,443
FILING DATE: 25-UL-1994
PROR APPLICATION DATA:
APPLICATION NUMBER: US 08/457,459
              Sequence 5682, Application US/09422978 Patent No. 6537751 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 GTATCTGAAGAGTCTG 21
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Matches 13, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-422-978-5682
-09-422-978-5682
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US-08-555-678-57
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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Cohen, Daniel

APPLICANT: Chumakov, Ilya

APPLICANT: Blumenfeld, Marta

APPLICANT: Blailelic markers for use in constructing a high density...

FILE REFERENCE: GENSET.020CP1

CURRENT APPLICATION NUMBER: US 00/9422,978

CURRENT APPLICATION NUMBER: US 09/229,850

EARLIER FILING DATE: 1999-04-21

EARLIER FILING DATE: 1999-11-23

EARLIER FILING DATE: 1998-11-23

EARLIER FILING DATE: 1998-04-21

NUMBER: OF SEQ ID NOS: 11796

SEQ ID NO 4659

LENTH: 19
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Patent No. 6770633;
GENERAL INFORMATION:
APPLICANT: Robbins, Joan M.
APPLICANT: Tritz, Richard;
TITLE OF INVENTION: RIBOZYME THERAPY FOR THE TREATMENT OF PROLIFERATIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; LOCATION: 1..19 To Stream amplification primer 99-16867 for SEQ 725, US-09-422-978-4659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 53.3%; Score 11.2; DB 1; Length 19; Best Local Similarity 81.2%; Pred. No. 2.4e+04; Matches 13; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4659, Application US/09422978
Patent No. 6537751
                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: unknown
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "primer"
FILING DATE: 01-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: BAK, MARY E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: WST45
TELECOMMUNICATION INFORMATION:
TELEFONE: 215-540-9206
TELEFAX: 215-540-9206
TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 81.2
Matches 13; Conservative
                                                                                                                                                                                                                                                                                        LENGTH: 19 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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; OTHER INFORMATION: Antisense Oligonucleotide US-09-488-671-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match
Best Local Similarity
Matches 13; Conserv
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; Batent No. 6770633
; Patent No. 6770633
; GENERAL INFORMATION:
    APPLICANT: Robbins, Joan M.
    APPLICANT: Tritz, Richard
    TITLE OF INVENTION: RIBOZYME THERAPY FOR THE TREATMENT OF PROLIFERATIVE
    TITLE OF INVENTION: SKIN AND EVE DISEASES
    FILE REFERENCE: 4960124.407
; CURRENT APPLICATION NUMBER: US/09/696,791
; CURRENT PILING DATE: 2000-10-25
; NUMBER OF SEQ ID NOS: 4523
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 467
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| Sequence 22, Application US/09488671A
| Patent No. 6187545
| GENERAL INFORMATION:
| APPLICANT: Robert McKay
| APPLICANT: Adecline W. Butler
| APPLICANT: Lex M. Cowsert
| TITLE OF INVENTION: ANTISENSE MODULATION OF PEPCK-CYTOSOLIC EXPRESSION
| TITLE OF INVENTION: ANTISENSE WOODLATION OF PEPCK-CYTOSOLIC EXPRESSION
| TITLE OF INVENTION: ANTISENSE WOODLATION OF PEPCK-CYTOSOLIC EXPRESSION
| TITLE OF INVENTION NUMBER: US/09/488,671A
| CURRENT FILING DATE: 2000-01-21
| SEQ ID NO 22
| LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , OTHER INFORMATION: Cdk4 ribozyme binding site US-09-696-791-467
                                                                                                                                                                                                                                                   , OTHER INFORMATION: Cdk4 ribozyme binding site US-09-696-791-466
      TITLE OF INVENTION: SKIN AND EYE DISEASES FILE REFERENCE: 480124.407 CURRENT APPLICATION NUMBER: US/09/696,791 CURRENT FILING DATE: 2000-10-25 NUMBER OF SEQ ID NOS: 4523 SOFTHARE: Patentin Ver. 2.0 SEQ ID NO 466 LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 GTATCTGAAGAGTCTG 21
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Best Local Similarity 81.2
Matches 13; Conservative
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                                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-488-671-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Robert McKay
APPLICANT: Madeline M. Butler
APPLICANT: Jacqueline Wyat

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Robert McKay
APPLICANT: Robert McKay
APPLICANT: Madeline M. Butler
APPLICANT: Jacqueline Wyatt
APPLICANT: Jacqueline Wyatt
APPLICANT: Lex M. Cowsert
TITLE OF INVENTION: ANTISENSE MODULATION OF PEPCK-CYTOSOLIC EXPRESSION
FILE REFRENCE: RTS-0123
CURRENT APPLICATION NUMBER: US/09/488,671A
CURRENT PILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 177
LENGTH: 20
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                                                                                                             Gaps
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Query Match
53.3%; Score 11.2; DB 3; Length 20;
Best Local Similarity 81.2%; Pred. No. 2.4e+04;
Matches 13; Conservative 0; Mismatches 3; Indels
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ORGANISM: Artificial Sequence
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RESULT 40

US-09-517-584A-86/c

j Sequence 86, Application US/09517584A

j Patent No. 6187587

j GENERAL INFORMATION:

j APPLICANT: Ian Popoff

j APPLICANT: Lex M. Cowsert

j APPLICANT: Lex M. Cowsert

j TITLE OF INVENTION: RTS-0121

CURRENT APPLICATION NUMBER: US/09/517,584A

CURRENT FILING DATE: 2000-03-22

NUMBER OF SEQ ID NOS: 89

j SEQ ID NOS: 89

j SEQ ID NOS 6

j LENGTH: 20

TYPE: DNA

OTHER INFORMATION: Antisense Oligonuclectide

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Search completed: August 12, 2005, 11:05:05 Job time: 97 secs

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Sequence 24, Appl
Sequence 94, Appl
Sequence 136, App
Sequence 166, App
Sequence 118, Appl
Sequence 129, Appl
Sequence 15, Appl
Sequence 15, Appl
Sequence 20, Appl
Sequence 20, Appl
Sequence 219, Appl
Sequence 199, Appl
Sequence 12, Appl
Sequence 2229, Appl
Sequence 2227, Appl
Sequence 222, Appl
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| US-10-10-10-919-31 |
| US-10-10-919-31 |
| US-10-10-919-944 |
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Sequence 448, App
Sequence 630, App
Sequence 64, Appl
Sequence 261, Appl
Sequence 10748, A
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1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/DS07_NEW_PUB.seq:*
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29: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
20: /cgn2_6/ptodata/2/pubpna/
                                          GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-848-754A-448
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US-10-619-739-630
US-10-109-36-64
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Listing first 100 summaries
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US-09-848-754A-1754/c

Sequence 1754, Application US/09848754A

Sequence 1754, Application No. US20030073207A1

Sequence 1754, Application No. US20030073207A1

GENERAL INFORMATION:
TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related TITLE OF INVENTION: Levels of Epidermal Growth Factor Receptors

TITLE OF INVENTION: Levels of Epidermal Growth Factor Receptors

TITLE OF INVENTION: Levels of Epidermal Growth Factor Receptors

FILE REFERENCE: MBHB00-958-1 (400/018)

CURRENT APPLICATION NUMBER: US/09/848,754A

NUMBER OF SEQ ID NOS: 9645

SEQ ID NO 1754

SEQ ID NO 1754
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                                        61.0%; Score 12.8; DB 10; Length 17; 87.5%; Pred. No. 1.7e+04; cive 0; Mismatches 2; Indels (
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Best Local Similarity 87.5%; Pred. No. 1.7e+04;
Matches 14; Conservative 0; Mismatches 2;
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Publication No. US20040175719A1
GENERAL INFORMATION:
TITLE OF INVENTION: Synthetic Tag Genes
FILE REFRENCE: 3502.1
CURRENT APPLICATION NUMBER: US/10/619,739
CURRENT FILING DATE: 2003-07-14
PRIOR APPLICATION NUMBER: 60/395,530
PRIOR PILING DATE: 2002-07-12
NUMBER OF SEQ ID NOS: 2068
SOFTWARE: FastERE for Windows Version 4.0
SEG ID NO 630
LENGTH: 20
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US-10-190-366-64
; Sequence 64, Application US/10190366
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ORGANISM: Artificial Sequence
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Best Local Similarity 87.5
Matches 14; Conservative
                                             Query Match
Best Local Similarity 87.5
Matches 14; Conservative
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ORGANISM: Homo sapiens
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US-09-848-754A-448/c
US-09-848-754A-448/c
Sequence 448, Application US/09848754A
Publication No. US20030073207A1
GENERAL INFORMATION:
APPLICANT RIDEXTWE Pharmaceuticals, Inc.
TITLE OF INVENTION: Levels of Epidermal Growth Factor Receptors
TITLE OF INVENTION: Levels of Epidermal Growth Factor Receptors
FILE REFERENCE: MBH800-958-I (400/018)
CURRENT APPLICATION VMBER: US/09/848,754A
CURRENT APPLICATION VMBER: 2001-05-03
NUMBER OF SEQ ID NOS: 9645
SOFTWARE: Patentin version 3.0
SEQ ID NO 448
                                                                                                                                                                                                                              Sequence 10747, A Sequence 10749, A Sequence 10752, A Sequence 156, App Sequence 157, App Sequence 4879, App Sequence 1817, App
                                                                     Sequence 4035, Ap
Sequence 5116, Ap
Sequence 5118, Ap
Sequence 5118, Ap
Sequence 5260, Ap
Sequence 5260, Ap
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US-09-864-636A-1817
US-09-864-426A-1817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Synthetic Oligonucleotide US-10-619-739-1019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-619-739-1019/C
Sequence 1019, Application US/10619739
Fublication No. US20040175719A1
GENERAL INFORMATION:
TITLE OF INVENTION: Synthetic Tag Genes
FILE REPERENCE: 3502.1
CURRENT APPLICATION NUMBER: US/10/619,739
CURRENT FILING DATE: 2003-07-14
PRIOR FILING DATE: 2002-07-12
NUMBER OF SEQ ID NOS: 2068
SOFTWARE: PastSEQ for Windows Version 4.0
SSOTTWARE: 20
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ORGANISM: Artificial Sequence
    TYPE: RNA
ORGANISM: Homo sapiens
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Gaps

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Length 21; Indels

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Sequence 10750, Application US/10847918

Sequence 10750, Application US/10847918

Publication No. US20050119210A1

GENERAL INFORMATION:

APPLICANT: Week

APPLICANT: Liu, Wei

APPLICANT: Liu, Wei

APPLICANT: Liu, Wei

APPLICANT: Howes, Steve

TITLE OF INVENTION: Compositions and Methods for Diagnosing and Treating Cancers

FILE REPERENCE: 201896-026000 (AM101264)

CURRENT FILING DATE: 2004-05-19

FRIOR PAPLICATION NUMBER: US/10/847,918

CURRENT FILING DATE: 2003-05-20

NUMBER OF SEQ ID NOS: 14937

SEQ ID NO 10750

LENGTH: 21

LENGTH: 21
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APPLICANT: Wisobing
APPLICANT: Bi, Xiaobing
APPLICANT: Liu, Weth
APPLICANT: Liu, Donna
APPLICANT: Liu, Donna
APPLICANT: Liu, Wisobing
APPLICANT: Storie, Donna
APPLICANT: Storie, Donna
APPLICANT: Howes, Steve
TITLE OF INVENTION: Compositions and Methods for Diagnosing and Treating Cancers
FILE REFERENCE: 031896-026000 (AMI01264)
CURRENT APPLICATION NUMBER: US/10/847,918
CURRENT FILING DATE: 2004-05-19
PRIOR FILING DATE: 2003-05-20
NUMBER OF SEQ ID NOS: 14937
SOFTWARE: PatentIn version 3.2
SEQ ID NO 10921
LENGTH: 21
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Pred. No. 2.8e+04;
0; Mismatches 1;
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; Publication No. US20050119210A1
; GENERAL INFORMATION:
SOFTWARE: Patentin version 3.2
SEQ ID NO 10748
LENGTH: 21
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Best Local Similarity 92.9%;
Matches 13; Conservative
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92.9%;
                                                                   TYPE: RNA
; ORGANISM: RNAi-sense strand
US-10-847-918-10748
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Best Local Similarity 92.9
Matches 13; Conservative
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US-10-847-918-10750
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; ORGANISM: Homo sapiens
US-10-847-918-10921
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APPLICANT: "Be, Xiaobing
APPLICANT: Liu, Wei
APPLICANT: Slown
APPLICANT: Slown
APPLICANT: Howes, Steve
TITLE OF INVENTION: Compositions and Methods for Diagnosing and Treating Cancers
TITLE OF INVENTION UNMER: 01896-056000 (AM101264)
CURRENT APPLICATION NUMBER: US/10/847,918
CURRENT FILING DATE: 2004-05-19
PRIOR APPLICATION NUMBER: US 60/471,729
PRIOR PLILING DATE: 2003-05-20
NUMBER OF SEQ ID NOS: 14937
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Sequence 261, Application US/10190366

Publication No. US20040006031A1

GENERAL INFORMATION:
APPLICANT: Nicholas M. Dean
APPLICANT: Susan M. Freier
APPLICANT: Kenneth W. Dobie
TITLE OF INVENTION: ANTISENSE MODULATION OF HMG-COA REDUCTASE EXPRESSION
FILE REFERENCE: PTS-0023
CURRENT APPLICATION NUMBER: US/10/190,366
CURRENT FILING DATE: 2002-07-02

NUMBER OF SEQ ID NOS: 409

SEQ ID NO 261
LENGTH: 20
                        GENERAL INFORMATION:

SEPPIGANT: Nicholas M. Dean
APPLICANT: Susan M. Preier
APPLICANT: Susan M. Preier
APPLICANT: Senach W. Dobie
TITLE OF INVENTION: ANTISENSE MODULATION OF HWG-COA REDUCTASE EXPRESSION
FILE REPERENCE: PTS-003.
CURRENT APPLICATION NUMBER: US/10/190,366
CURRENT FILING DATE: 2002-07-02
SEQ ID NOS: 409
SEQ ID NO 64
LENGTH: 20
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Pred. No. 2.8e+04;
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                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Antisense Oligonucleotide US-10-190-366-64
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Ublication No. US20050119210A1
GENERAL INFORMATION:
APPLICANT: Wyeth
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92.9%;
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       Publication No. US20040006031A1
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Best Local Similarity 92.93
Matches 13; Conservative
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ORGANISM: H. sapiens
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US-10-847-918-10748/C
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OTHER INFORMATION: Antisense Oligonucleotide
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82.4%;
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Best Local Similarity 82.4<sup>†</sup>
Matches 14<sup>‡</sup>, Conservative
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Best Local Similarity 82.4'
Matches 14; Conservative
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; ORGANISM: Homo sapiens
US-09-848-754A-449
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US-10-167-034-78/c
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                                                                                                                                                                                                                                                                                APPLICANT: Wyeth
APPLICANT: Be, Xiaobing
APPLICANT: Liu, Wei
APPLICANT: Liu, Wei
APPLICANT: Liu, Wei
APPLICANT: Liu, Wei
APPLICANT: Howes, Steve
TITLE OF INVENTION: Compositions and Methods for Diagnosing and Treating Cancers
FILE REFERENCE: 011896-026000 (AM101264)
CURRENT APPLICATION NUMBER: US/10/847,918
CURRENT APPLICATION NUMBER: US 60/471,729
PRIOR FILING DATE: 2004-05-10
NUMBER OF SEQ ID NOS: 14937
SEQ ID NOS: 14937
SEQ ID NO 10922
LENGTH: 21
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APPLICANT: Weth
APPLICANT: Liu, Weth
APPLICANT: Slonim, Donna
APPLICANT: Slonim, Donna
APPLICANT: Howes, Steve
TITLE OF INVENTION: Compositions and Methods for Diagnosing and Treating Cancers
FILE REFERENCE: 031896-026000 (AM101264)
CURRENT APPLICATION NUMBER: US/10/847,918
CURRENT APPLICATION NUMBER: US 60/471,729
PRIOR FILING DATE: 2003-05-20
NUMBER OF SEQ ID NOS: 14937
SOFTWARE: PatentIn version 3.2
SEQ ID NO 10923
LENGTH: 21
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      Score 12.4; DB 21; Length 21;
Pred. No. 2.8e+04;
0; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 21; Length 21;
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Pred. No. 2.8e+04;
0; Mismatches 1
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Publication No. US20050119210A1
GENERAL INFORMATION:
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        59.0%;
92.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59.0%;
92.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: RNA
ORGANISM: RNAi-sense strand
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Ouery Match
Best Local Similarity 92.9'
Matches 13; Conservative
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Best Local Similarity 92.9
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Matches 9, Conserv
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; Sequence 449, Application US/09848754A
; Publication No. US20030073207A1
; GENERAL INFORMATION:
    APPLICANT: Ribozyme Pharmaccuticals, Inc.
    TITLE OF INVENTION: Levels of Epidermal Growth Factor Receptors
    TITLE OF INVENTION: Levels of Epidermal Growth Factor Receptors
    TITLE OF INVENTION: Levels of Epidermal Growth Factor Receptors
    TURRENT APPLICATION NUMBER: US/09/848,754A
    CURRENT FILING DATE: 2001-05-03
    NUMBER OF SEQ ID NOS: 9645
    SOFTWARE: Patentin Version 3.0
    SEQ ID NO 449
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Publication No. US20030228690A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Brenda F. Baker
APPLICANT: Susan M. Freier
APPLICANT: Kenneth W. Dobie
TITLE REFERENCE: PTS-0003
CURRENT APPLICATION NUMBER: US/10/167,034
CURRENT FILING DATE: 2002-06-10
NUMBER OF SEQ ID NOS: 142
SEQ ID NO 78
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Publication No. US20030114401A1
| GENERAL INFORMATION:
| APPLICANT: C. Frank Bennett
| APPLICANT: Susan M. Freier
| TITLE OF INVENTION: ANTISENSE MODULATION OF SHIP-1 EXPRESSION
| FILE REFERENCE: RTS-0256
| CURRENT APPLICATION UNBER: US/10/003,919
| CURRENT FILING DATE: 2001-12-06
| NUMBER OF SEQ ID NOS: 87
| LENGTH: 20
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Pred. No. 3.5e+04;
0; Mismatches 3;
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1 CTGGCGTATCTGAAGAGTCT 20
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1 CUGAGGCAUCUCAAGACUCU 20
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SOFTWARE: PatentIn version 3.2
SEQ ID NO 46408
                                                                                                                                                                                                                                                                                                                                         ); ORGANISM: RNAi-sense strand US-10-786-720-13349
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Best Local Similarity 75.0
Matches 15; Conservative
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Matches 10; Conserv
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US-10-751-736-46408/c
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US-10-751-736-46777/c
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                                                                                                                                                                                                                                                                                                                                 Sequence 29, Application US/10317500

Publication No. US20040115637A1

GENERAL INFORMATION:
APPLICANT: Robert McKsy

APPLICANT: Remeth W. Dobie
TITLE OF INVENTION: MODULATION OF PPAR-ALPHA EXPRESSION
FILE REFERENCE: RTS-0380

CURRENT APPLICANTON NUMBER: US/10/317,500

CURRENT FILING DATE: 2002-12-11

NUMBER OF SEQ ID NOS: 276

LENGTH: 20
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US-10-317-500-184
; Sequence 184, Application US/10317500
; Publication No. US20040115637A1
; GENERAL INFORMATION:
; APPLICANT: Robert MCKAY
; TITLE OF INVENTION: MODULATION OF PPAR-ALPHA EXPRESSION
; FILE REFERENCE: RTS-0380
; CURRENT APPLICATION WUMBER: US/10/317,500
; CURRENT FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 276
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100.0%; Pred. No. 4.4e+04;
iive 0; Mismatches 0;
                                                                       ; OTHER INFORMATION: Antisense Oligonucleotide
US-10-167-034-78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , OTHER INFORMATION: Antisense Oligonucleotide US-10-317-500-29
                                                                                                                                                                                                           4 GCGTATCTGAAGAGTCT 20
                 TYPE: DNA
ORGANISM: Artificial Sequence
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17 GCGTAGCTGGAGGGTCT 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Artificial Sequence
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Matches 12; Conservative
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US-10-317-500-29/c
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LENGTH: 20
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                                                       FEATURE:
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RESULT 17
US-10-786-720-13349
is guamence 13349, Application US/10786720
is guamence 13349, Application US/10786720
is guamence 13349, Application No. US20040191818A1
is guamence 13349, Application No. US20040191818A1
is guamence 13349, Application No. US20040191818A1
is applicant: Wyeth
is APPLICANT: Wyeth
is APPLICANT: Liu, Wei
is TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING AUTOIMMUNE
is TITLE OF INVENTION: USSASSE
is FILE REFERENCE: 031896-023000 (AM101331L)
is CURRENT PAPLICATION UNBER: US/10/786,720
is CURRENT PLING DATE: 2004-02-26
is NUMBER OF SEQ ID NOS: 21135
is SEQ ID NO 13349
is LENGTH: 21
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Publication No. US20040265230A1

GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Martinez, Robert
APPLICANT: Brown, Eugene
APPLICANT: Liu, Wei,
APPLICANT: Liu, Wei
APPLICANT: Liu, Wei
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Martinez, Robert
APPLICANT: Brown, Bugene
APPLICANT: Liu, Wei
TILLE CANT: Liu, Wei
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON
TITLE OF INVENTION: CANCERS
FILE REFERENCE: AM100927 (031896-002000)
CURRENT APPLICATION NUMBER: 2003-01-06
PRIOR APPLICATION NUMBER: US Provisional Application 60/438,000
PRIOR FILING DATE: 2003-01-06
PRIOR FILING DATE: 2003-01-06
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Pred. No. 4.4e+
0; Mismatches
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Sequence 447, Application US/09848754A

Publication No. US20030073207A1

GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals, Inc.

TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate

TITLE OF INVENTION: Levels of Epidermal Growth Factor Receptors

TITLE OF INVENTION: Levels of Epidermal Growth Factor Receptors

CURRENT APPLICATION NUMBER: US/09/848,754A

CURRENT FILING DATE: 2001-05-03

SOFTWARE: Patentin version 3.0

SEQ ID NO 447
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Publication No. US20030092646A1

GENERAL INPORMATION:

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: Blatt, Larry

APPLICANT: McSwiggen, Jim

TITLE OF INVENTION Method and Reagent for the Inhibition of CD20

FILE REFERENCE: 400/010

CURRENT FILING DATE: 2001-02-09

PRIOR APPLICATION NUMBER: US/09/780,164

PRIOR APPLICATION NUMBER: US/09/780,164

MUMBER OF SEQ ID NOS: 2603

SOFTWARE: PatentIn version 3.0

LENGTH: 17
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86.7%; Pred. No. 5.5e+04;
tive 0; Mismatches 2;
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86.7%; Pred. No. 5.5e+04;
live 0; Mismatches 2;
                                                                                                                  Query Match 56.2%; Score 11.8; DB 19; Best Local Similarity 73.3%; Pred. No. 5.5e+04; Matches 11; Conservative 2; Mismatches 2;
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Best Local Similarity 86...
Best Local 3; Conservative
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Best Local Similarity 86.7
Matches 13; Conservative
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ORGANISM: Homo sapiens
US-09-780-164-577
                         TYPE: RNA
ORGANISM: Homo sapiens
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US-09-848-754A-447
                                                                                                                                                                                                                                                                                                                                                                     US-09-848-754A-447/C
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US-09-780-164-577/C
                                                                      US-10-287-949A-5737
LENGTH: 16
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Publication No. US20040102389A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICAMY: Ribozyme Pharmaceuticals, Inc.
APPLICAMY: Ribozyme Pharmaceuticals, Inc.
APPLICAMY: Baveo, Pam
APPLICAMY: Stinchcomb, Dan
APPLICAMY: Escobedo, Jaim
APPLICAMY: Escobedo, Jaim
APPLICAMY: Escobedo, Jaim
APPLICAMY: Escobedo, Jaim
APPLICAMY: William Stinchcomb, Dan
APPLICAMY: Levels of Vascular Endothelial Growth Factor Receptor
TITLE OF INVENTION NUMBER: US/10/287, 949A
CURRENT APPLICATION NUMBER: US/10/287, 949A
CURRENT PELING DATE: 2003-04-11
SUMMER OF SEQ ID NOS: 20822
SOFTWARE: Patentin version 3.0
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Publication No. US20040077555A1

GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: Bavco. Pam

APPLICANT: Bavco. Pam

APPLICANT: Stinchcomb, Dam

APPLICANT: Escobedo, Jaime

TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re

TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re

TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases

TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases

CURRENT FILING DATE: 2002-05-03

NUMBER OF SEQ ID NOS: 20822

SOFTWARE PatentIn version 3.0

LENGTH: 16
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                 FILE REFERENCE: ANIO0227 (031996-002000)
CURRENT APPLICATION NUMBER: US/10/751,736
CURRENT FILING DATE: 2003-01-06
PRIOR APPLICATION NUMBER: US Provisional Application 60/438,000
PRIOR FILING DATE: 2003-01-06
NUMBER OF SEQ ID NOS: 54873
SEQ ID NO 46777
LENGTH: 21
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                                                                                                                                                                                                                                                                                                                                      57.1%; Score 12; DB 20; Length 21; 75.0%; Pred. No. 4.4e+04; ive 0; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                              2 TGGCGTATCTGAAGAGTCTG 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20 TGTCCTCTCTGATGAGGCTG 1
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                                                                                                                                                                                                                                                                                                                                                                     l Similarity 75.0
15; Conservative
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                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: homo sapiens
US-10-751-736-46777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Homo sapiens
US-10-138-674-5737
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Best Local Similarity
'-hag 11; Conservat
  TITLE OF INVENTION:
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Best Local
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Page 7

TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor; TITLE REFERENCE: MBHB00-876-N (400/049); FILE REFERENCE: MBHB00-876-N (400/049); CURRENT APPLICATION NUMBER: US/10/287,949A; CURRENT APPLICATION NUMBER: US/204-11; NUMBER OF SEQ 1D NOS: 20822; SOFTWARE: PatentIn version 3.0 SEQ 1D NO 4438
LENGTH: 17

TYPE: ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Parco, Pam
APPLICANT: McSwiggen, Jim
APPLICANT: McSwiggen, Jim
APPLICANT: Stinchcomb. Dan
APPLICANT: Stinchcomb. Dan
APPLICANT: Stinchcomb. Dan
APPLICANT: Stinchcomb. Dan
APPLICANT: Scobedo, Jaine
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
FILE REPERENCE: MBHB00-876-N (400/049)
CURRENT APPLICATION NUMBER: US/10/287,949A
CURRENT APPLICATION NUMBER: US/10/287,949A
CURRENT APPLICATION STILING DATE: 2003-04-11
NUMBER OF SEQ ID NOS: 20822
SOFTWARE: Patentin version 3.0
SEQ ID NO 7389
LENGTH: 17
TYPE: RNA
ORGANISM: Homo sapiens
US-10-287-949A-7389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Pavco, Pamela
APPLICANT: Sandberg, Jennifer
APPLICANT: Sandberg, Jennifer
APPLICANT: Sandberg, Jennifer
APPLICANT: Gordon, Gilad
APPLICANT: Stinchcomb, Dan
TITLE OF INVENTION: NUCLEIC ACID BASED MODULATION OF VASCULAR ENDOTHELIAL GROWTH FACT
TITLE OF INVENTION: NUCLEIC ACID BASED MODULATION OF VASCULAR ENDOTHELIAL GROWTH FACT
TITLE OF INVENTION: RECEPTOR FOR THE TREATMENT OF ANGIOGENESIS RELATED DISEASES AND
FILE REFERENCE: MEHBOZ-325PCT (400/047)
CURRENT APPLICATION NUMBER: US/10/712,633
CURRENT FILING DATE: 2003-11-13
PRIOR APPLICATION NUMBER: US 60/005,974
PRIOR FILING DATE: 1995-10-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 56.2%; Score 11.8; DB 19; Best Local Similarity 73.3%; Pred. No. 5.5e+04; Matches 11; Conservative 2; Mismatches 2;
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Publication No. US20040220128A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 GGCGTATCTGAAGAG 17
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1 GACGUAACUGAAGAG 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: RNA
CORGANISM: Homo sapiens
US-10-287-949A-4438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 27
US-10-287-949A-7389
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                                                                                                                                                                                                                                                                                     Sequence 4438 Application US/10138674
; Sequence 4438
; Bublication No. US20040077565A1
; GENERAL INFORMATION:
   APPLICANT: Ribozyme Pharmaceuticals, Inc.
   APPLICANT: Bavco, Pam
   APPLICANT: Brinchcomb, Dan
   APPLICANT: Stinchcomb, Dan
   APPLICANT: Scobedo, Jaime
   APPLICANT: Stinchcomb, Dan
   APPLICANT: Scopedo, Jaime
   APPLICANT: Scopedo, Jaime

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US-10-138-674-7389
US-10-138-674-7389
US-10-138-674-7389
Sequence 7389, Application US/10138674
Publication No. US20040077565A1
GENERAL INFORMATION:
APPLICANT: Pavco, Pam
APPLICANT: APLOCOMD, Dan
APPLICANT: Estochedo, Jaime
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions RefILE REFERENCE: MBHB00-876-N (400/049)
CURRENT APPLICATION NUMBER: US/10/138,674
CURRENT PILIC DATE: 2002-05-03
NUMBER OF SEQ ID NOS: 20822
SOFTWARE: Patentin Version 3.0
SEQ ID NO 1889
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56.2%; Score 11.8; DB 18; Length 17;

Best Local Similarity 73.3%; Pred. No. 5.5e+04;

Matches 11; Conservative 2; Mismatches 2; Indels C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 26
US-10-287-949A-4438
Sequence 4438, Application US/10287949A
Publication No. US20040102389A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.;
APPLICANT: Pavco, Pam
APPLICANT: McSwiggen, Jim
APPLICANT: Stinchcomb, Dan
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1 GACGUAACUGAAGAG 15
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Matches 11; Conservative
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; ORGANISM: Homo sapiens
US-10-138-674-7389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens US-10-138-674-4438
                                                                                                                                                                                                                                                                                     US-10-138-674-4438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: RNA
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US-10-174-319-94
; Sequence 94, Application US/10174319
; Publication No. US20030232771A1
; GENERAL INFORMATION:
; APPLICANT: Donna T. Ward
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               56.2%;
                                                                      TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                        3 GGCGTATCTGAAGAG 17
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                                                                                                                                                                                                                      Best Local Similarity 86.7
Matches 13; Conservative
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Best Local Similarity 86.7
Matches 13; Conservative
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Matches 13; Conservative
        NUMBER OF SEQ ID NOS: 121
SEQ ID NO 24
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: H. sapiens
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US-10-174-319-94
                                                                                                                                                           US-10-174-319-24
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; Sequence 38, Application US/10181991
; Publication No. US20030211609A1
; GRNERAL INFORMATION:
    APPLICANT: Lex M. Cowsert
; APPLICANT: Lex M. Cowsert
; APPLICANT: Lex M. Cowsert
; TITLE OF INVENTION: ANTISENSE MODULATION OF ARA70 EXPRESSION
; CURRENT APPLICATION NUMBER: US/10/181,991
; CURRENT FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: 09/488,857
; RIOR APPLICATION NUMBER: 09/488,857
; RIOR RILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 38
; LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   56.2%; Score 11.8; DB 17; Length 20; 86.7%; Pred. No. 5.6e+04; tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 17;
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1Sequence 24, Application US/10174319

1 Publication No. US2003023771A1

2 GENERAL INFORMATION:

APPLICANT: Susan M. Freier

APPLICANT: Kenneth W. Dobie

TITLE OF INVENTION: ANTISENSE MODULATION OF MARK3 EXPRESSION

FILE REPRENCE: PTS-0018

CURRENT APPLICATE: 2002-06-17
                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 11.8; DB 20;
Pred. No. 5.5e+04;
2; Mismatches 2;
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PRIOR APPLICATION NUMBER: US 08/584,040
PRIOR FILING DATE: 1996-01-08
PRIOR APPLICATION NUMBER: US 09/371,772
PRIOR FILING DATE: 1999-08-10
PRIOR FILING DATE: 2090-01-07
PRIOR FILING DATE: 2000-11-07
PRIOR FILING DATE: 2001-05-29
PRIOR FILING DATE: 2001-05-29
PRIOR FILING DATE: 2001-05-39
PRIOR FILING DATE: 2001-05-03
NUMBER OF SEQ ID NOS: 5989
SOFTWARE: PATENTIN VERSION 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                    56.2%;
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Best Local Similarity 73.3
Matches 11; Conservative
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Matches 13; Conservative
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US-10-712-633-339
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                                                                                                                                                                                                                                                                                                                                                     TYPE: RNA
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Sequence 1366, Application US/10289762

Publication No. US20040006218A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prever TITLE OF INVENTION: and treatment of infection
FILE REFERENCE: 9710-003-999
CURRENT APPLICATION NUMBER: US/10/289,762
CURRENT FILING DATE: 2003-03-27

NUMBER OF SEQ ID NOS: 6849

SEQ ID NO 1366
LENGTH: 20
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                                                                                    Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Susan M. Freier
APPLICANT: Kenneth W. Dobie
TITLE OF INVENTION: ANTISENSE MODULATION OF MARK3 EXPRESSION
FILE REFERENCE: PTS-0018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                 Indels
                                                                                    56.2%; Score 11.8; DB 17;
86.7%; Pred. No. 5.6e+04;
tive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 11.8; DB 17;
Pred. No. 5.6e+04;
FEATURE: OTHER INFORMATION: Antisense Oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/174,319
CURRENT FILING DATE: 2002-06-17
NUMBER OF SEQ ID NOS: 121
SEQ ID NO 94
LENGTH: 20
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APPLICANT: Barany, Francis
APPLICANT: Barany, Francis
APPLICANT: Liu, Jianzhao
APPLICANT: Liu, Jianzhao
APPLICANT: Liu, Jianzhao
APPLICANT: Zirvi, Monib
APPLICANT: Zirvi, Monib
APPLICANT: Paty, No. US20030190634Alman P.
APPLICANT: Paty, Philip B.
TITLE OF INVENTION: POLYMORPHISMS AND ALIGNMENT OF CLONES IN GENOMIC
TITLE OF INVENTION: SEQUENCING
FILE REFERENCE: 19603/2621
TITLE OF INVENTION: SEQUENCING
FILE REFERENCE: 19603/2621
CURRENT APPLICATION NUMBER: US/10/198,235
CURRENT FILING DATE: 2000-01-05
PRIOR APPLICATION NUMBER: 60/114,881
PRIOR APPLICATION NUMBER: 60/114,881
PRIOR PILING DATE: 1999-01-06
NUMBER OF SEQ ID NOS: 181
SEQ ID NO 118
LENGTH: 21

LENGTH: 21

LENGTH: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , OTHER INFORMATION: Description of Artificial Sequence: probe/primer US-10-198-235-118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 56.2%; Score 11.8; DB 16; Length 21; Best Local Similarity 86.7%; Pred. No. 5.6e+04; Matches 13; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    squence 862, Application US/10643775

publication No. US200S0026156A1

GENERAL INFORMATION:
APPLICANT: Lie, Oystein
APPLICANT: Lie, Oystein
APPLICANT: Lingaas, Frode
TITLE OF INVENTION: Varification of Food Origin Based on
TITLE OF INVENTION: Varification of Food Origin Based on
FILE REFERENCE: 66849-019
CURRENT APPLICATION NUMBER: US/10/643,775
CURRENT PILING DATE: 2003-08-18
PRIOR APPLICATION NUMBER: US 60/404,200
PRIOR FILING DATE: 2002-08-16
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86.7%; Pred. No. 5.6e+04;
tive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 1377
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 862
LENGTH: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 129, Application US/09752983; Patent No. US20010016575A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Oreochromis niloticus
                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 GGCGTATCTGAAGAG 17
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Best Local Similarity 86.74
Matches 13, Conservative
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                                                         Sequence 87, Application US/10766185

Sequence 87, Application US/10766185

Publication No. US20040152655A1

GENERAL INFORMATION:

APPLICANT: Yoon, Heejeong

APPLICANT: And, Lingjun

APPLICANT: Jiang, Xiaoming

TITLE OF INVENTION: Antisense Oligonucleotides that inhibit expression of HIF-1

FILE REFERENCE: REX 7034

CURRENT APPLICANT: NUMBER: US/10/766,185

CURRENT APPLICATION NUMBER: US/10/766,185

CURRENT APPLICATION NUMBER: US/10/766,185

CURRENT PILING DATE: 2004-01-28

NUMBER OF SEQ ID NOS: 130

SEQ ID NO 87

LENGTH: 20
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Pred. No. 5.6e+04;
O: Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ), OTHER INFORMATION: antisense oligonucleotide US-10-766-185-87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Synthetic Construct
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                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 86.7%;
Matches 13; Conservative
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Matches 13; Conservative
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US-10-198-235-118/c
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Gaps

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; Sequence 118, Application US/10198235; Publication No. US20030190634A1

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0; Mismatches
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                                                                                                                                                                             21
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ORGANISM: Artificial Sequence
                                                                                                                                                                               4 GCGTATCTGAAGAGTCTG
                                                                                     Query Match
Best Local Similarity 77.8
Matches 14; Conservative
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Best Local Similarity 77.8
Matches 14; Conservative
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Fatent No. US20020137215A1

GENERAL INFORMATION:

APPLICANT: Francis, Kevin P.

APPLICANT: Francis, Anthony F.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR USE THEREOF IN MODIFYING

TITLE OF INVENTION: US/09/888, 049

CURRENT APPLICATION NUMBER: US/09/888, 049

CURRENT APPLICATION NUMBER: 60/216, 257

PRIOR APPLICATION NUMBER: 60/216, 257

PRIOR APPLICATION NUMBER: 60/214, 105

PRIOR FILING DATE: 2001-06-21

PRIOR FILING DATE: 2001-07-06

PRIOR FILING DATE: 2001-03-07

NUMBER OF SEQ ID NOS: 20

SEQ ID NO 15

LENGTH: 20
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GENERAL INFORMATION:
APPLICANT: Loren J. Miraglia, Pamela Nero, Mark J.
APPLICANT: Graham, Brett P. Monia
TITLE OF INVENTION: ANTISENSE MODULATION OF HUMAN MDM2
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 271
CORRESPONDENCES. 271
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Jane Massey Licata
                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE COMPUTER: IBM PC PERATING SYSTEM: WINDOWS 95 SOFTWARE: WORDPERFECT 6.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/752,983 FILING DATE: 02-Jan-2001
                                                                                                                                             SSEB: Law Offices of Jane Massey Licata
F: 66 East Main Street
Marlton
                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: ...
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/280,805
FILING DATE: -Unknown>
ATTORNEY/ABENT INFORMATION:
NAME: Licata, Jane Massey,
REGISTRATION NUMBER: 32,257
REGISTRATION NUMBER: ISPH-0
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELERAX: 609-810-1454
INFORMATION FOR SEQ ID NO: 129:
SEQUENCE CHARACTER STICS:
LENGTH: 20 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14; Conservative
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MEDIUM TYPE: DISKETT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                        STATE: NJ
COUNTRY: U.S.A.
ZIP: 08053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 38
US-09-888-049-15/c
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US-101-094-146-4/c
| Sequence 4, Application US/10094146
| Sequence 4, Application US/10094146
| Sequence 4, Application No. US20020192755A1
| GENERAL INVORMATION:
| APPLICANT: FRANCIS, Kevin P.
| APPLICANT: DOYLE, Timothy C.
| APPLICANT: MAWOTKA, Kevin P.
| TITLE OF INVENTION: METHODS OF SCREENING FOR INTRODUCTION OF DNA INTO A.
| TITLE OF INVENTION: METHODS OF SCREENING FOR INTRODUCTION OF DNA INTO A.
| TITLE OF INVENTION: METHODS OF SCREENING FOR INTRODUCTION OF DNA INTO A.
| FILE REFERENCE: 9400-0015 / PXE-015.US CURRENT FILING DATE: 2002-06-10
| PRIOR FILING DATE: 2001-06-10
| PRIOR FILING DATE: 2001-03-07 |
| PRIOR FILING DATE: 2001-03-07 |
| PRIOR FILING DATE: 2001-05-22 |
| NUMBER OF SEQ ID NOS: 35 |
| SOFTWARE: PATENTIN Ver. 2.0 |
| SEQ ID NO 4 |
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US-10-093-365-20/C

US-10-093-365-20/C

Sequence 20, Application US/10093365

Publication No. US2030099962A1

GENERAL INFORMATION:

APPLICANT: Schernthaner, Johann

APPLICANT: Piche, Caroline

APPLICANT: Robert, Laurian

TITE OF INVENITON: Methods to Isolate Gene Coding and Flanking DNA

FILE REFRENCE: 0811.1200001

CURRENT FILING DATE: 2002-03-08

FRIOR APPLICATION NUMBER: US/10/093,365

CURRENT FILING DATE: 2001-03-09

NUMBER OF SEQ ID NOS: 47

SOFTWARE: Patentin version 3.1

SEQ ID NO 20

LENTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Description of Artificial Sequence: primer LuxA-Rev
US-10-094-146-4
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; OTHER INFORMATION: Description of Artificial Sequence: Primer; OTHER INFORMATION: LuxA-Rev
US-09-888-049-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 20;
                                                                                                                   55.2%; Score 11.6; DB 9; Length 20; 77.8%; Pred. No. 7e+04; tive 0; Mismatches 4; Indels
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Pred. No. 7e+04;
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0; Gaps

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AZ818271 2M0088M08 AG199044 Pan trog1 AG203835 Pan trog1 AZ787920 2M0034M09	CL694050 PKI01638 CL423467 01S0557-0 AJ662026 AJ662026	AJ588865 Arabidops AZ358656 IM0101K12 BQ595520 E012693-0	AZ320114 1M0040D05 AZ436082 1M0233A10 AZ772787 1M0583M24	AZ807038 2M0069C06 CL436802 PST3869-N	BG927412 HNC1-1-G1 BG924475 HNC27-1-D	D11800 HUMHWOLKSTZ D11801 HUMHWOLHOI	D11803 HOWHWO2B04 D11818 HUMHMO2B04 BG928185 HNC65-1-D	BG900971 HOA52-1-C	BG924473 HNC27-I-D BG928126 HNC65-I-B CD532195 2648 Arab	CO779101 BL005C F0 AZ316351 1M0034A11	AZ619410 1M0451F11 AZ649987 1M0519J21	AZ817897 2M0087D09 AZ835078 2M0129E07	CO792195 NT014B H0 AZ511294 1M0356G16	AZ607204 1M0429H03 AZ623540 1M0461G23	AZ875020 ZM0189BZ4 AG203054 Pan trog1	AJ649143 AJ587324 Arabidops	AJ592301 Arabidops CF317235 HD06-N1	CO792214 NT014C A1 AZ490612 1M0323L11	AZ508355 1M0350013 AZ795136 2M0049A16	AZ834391 2M0117N04 CL668704 PRI0158b	BQ593485 S015529-0 AZ475341 1M0293H11	AZ610524 1M0435B21	AG190598 Pantrog1	AUS8/844 AIRDIUUDB AUS6271 AUS6271	AZ331625 1M0059M07 AZ346766 1M0082H08	AZ510119 1M0354123	AZ628010 1M04/5K09 AZ819244 2M0089F14	AZ820567 2M0092B19 AZ875300 2M0189D22	AJS98221 Arabidops	EG92/923 HNC45-1-E C01992 HUMGS000401	CL678657 PRI0123C_ AB088509 AB088509_	CO794844 NT144D B0	AZ774829 2M0004D10	AU287572 AU257572
8 AZ818271 9 AG199044 9 AG203835 8 AZ787920	o ο -	1000	80 80 80	80 60	441		- 1- 4	44	444	0 ~ 0	60 60	6 60	8	ω ω	დ თ	ч б	۷ و	6	ထထ	ω σ	N G	000	00	ף ע	α α	ο Φ	ω ω	ω α	00	4 0	ο .	1 2 0	0 00	5 1
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GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compuge	leic search, using sw model	August 12, 2005, 09:55:08 ; Search t (without a 442.608 M	US-09-743-825-8	1 ctggcgtatctgaagagtctg 21	IDENTITY NUC Gapop 10.0 , Gapext 1.0	34239544 seqs, 19032134700 residues	hits satisfying chosen parameters:	ength: 0 ength: 21	ım Match	Maximum Match 100% Listing first 100 summaries	ເນັ					s the number of results predi	er than or equal to the score	SUMMARIES		Match Length DB ID	20.	21 6	19 19	20 8	500	8 8 70 70 8	10 9	50 50 50 50 50 50 50 50 50 50 50 50 50 5	21 4	20 6	20 7	19 1 19 7	8 8 70 8	
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VERSION

KEYWORDS SOURCE

RESULT 1 AZ784664

98 99 100

REFERENCE AUTHORS JOURNAL

COMMENT

TITLE

FEATURES

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Direct Submission

Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue
Gaston Cremieux, 91057 Evry cedex, FRANCE
PCR was performed on DNA from transformants of Arabidopsis thaliana
plants from INRA (Versailles). The DNA fragment(s) resulting from
the PCR were directly sequence from the left or the right border
to determine the genomic sequence flanking the insertion. T-DNA
derived sequences were removed. Information to order the
corresponding mutant line and a link to a database providing a
graphical display of the insertion site are available at
http://dbsgap.versailles.inra.fr/publiclines/. This sequence has
been generated in the framework of the French plant genomics
program 'Genoplante' (http://www.genoplante.com and
http://genoplante-info.info.infologen.fr).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CA851013 21 bp mRNA linear EST 01-AUG-2003 D09B11 C11_04.abl cDNA Peking library 2, 4 day SCN3 Glycine max cDNA clone_D09B11 5', mRNA sequence.
                                                                                                                                                                                                                          Arabidopsis thaliana T-DNA flanking sequence, right border, clone 631B09, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Brunaud, V., Balzergue, S., Dubreucq, B., Aubourg, S., Samson, F., Chauvin, S., Bechtold, N., Cruaud, C., DeRose, R., Pelletier, G., Lepiniec, L., Caboche, M. and Lecharny, A.

T-DNA integration into the Arabidopsis genome depends on sequences
                                                                                                                                                                                                                                                                                                                                                                     AJ592729.1 GI:37942353
AZ592729.1 GI:37942353
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Arabidopsis thaliana
Bukaryotas, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     clone_lib="Arabidopsis thaliana T-DNA insertion lines"
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80.0%; Pred. No. 2.2e+06;
iive 0; Mismatches 3;

    15
/note="T-DNA flanking sequence"

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/cultivar="Wassillewskija"
/db_xref="taxon:3702"
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  Best Local Similarity 91.7
Matches 11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Wm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
                                                                                                                                                                                                                                                                   AZ784664 100 20 bp DNA linear GSS 16-FEB-2001 2M0027IIOR Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC2M0027IIO R, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 20)
Dunn, D., Aoyagi, Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Menen, B., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
     CO788185 NT003C_A1
AZ393342 1M0156C21
AZ441394 1M0233P05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /lab_host="E. Coli strain XLIO-Gold, Tl-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42Ivv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0027 row: I column: 10
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Seg primer: CACACAGGAAACAGCTATGACC
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Location/Qualifiers
     CO788185
AZ393342
AZ441394
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Length 20;

49.5%; Score 10.4; DB 8;

Query Match

ORIGIN

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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMAQ2 (gill #1732114|gb]AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xilio-Gold (Stratagene) cells and selected for ampicillin resistance."
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2M0190A02R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGC2M0190A02 R, genomic survey sequence.
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Dunn, D., Aoyagi, A., Barber, M., Meacorn, T., Duval, B., Hamil, C., Islam, H., Longarer, S., Mahmoud, M., Menen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weise, R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                  /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCNM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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Std Error: 0.00
                      Plate: 0331 row: N column: 22
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers
                                                                                                                                                                                  organism="Mus musculus"
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University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                  /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                     /db_xref="taxon:10090"
/clone="UUGC1M0331N22"
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
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Insert Length: 10000
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84112, USA
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                                                                                                                                                                                                                                           Alkharouf, N.W., Khan, R. and Matthews, B.F.
Alkharouf, N.W., Khan, R. and Matthews, B.F.
Analysis of expressed sequence tags from roots of resistant soybean unfected by the soybean cyst nematode
Unpublished (2002).
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
                                                                                                                                                                                                                                                                                                                                                                                                             Soybean Genomics and Improvement Laboratory (SGIL)
US Department of Agriculture (USDA), ARS, PSI
Bldg.006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="D09B11"
/tissue_type="Roots"
/dev_stage="Seedlings"
/clone_liber_type="Seedlings"
/clone_tiber_tobAx Peking library 2, 4 day SCN3"
/note="Vector: pBluescript SK-; cDNA clones from mRNA
extracted from Peking roots 2 and 4 days past invasion."
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84112, USA
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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Fax: 301 504 5752
Email: alkharon@ba.ars.usda.gov.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Glycine max"
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/cultivar="Peking"
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Mus musculus
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CA851013.1 GI:33387806
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Fax: 801 585 7177
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/lab hose=""" (lab hose=""" wate" / lab hose=""" cloi strain XLIO-Gold, T1-resistant, F-" / Clone lib="Wouse 10kb plasmid UUGCIM library" / note="Weetor: PWD42nv; Purified genomic DNA From M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resources (documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XLIO-Gold (Stratagene) cells and selected for ampicillin resistance."
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PRI0130b_G06_2 - PRI0130b.BR (17) Mixed stage fosmid library of P.
pacificus var. California Pristionchus pacificus genomic, genomic
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Pristionchus pacificus
Pristionchus pacificus
Bukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.

(bases 1 to 17)
Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
AppaDB: an AcedB database for the nematode satellite organism
Pristionchus pacificus
Nucleic Acids Res. 32 (1), D421-D422 (2004)
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This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
Seq primer: T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
45.7%; Score 9.6; DB 8; Length 20;
Best Local Similarity 75.0%; Pred. No. 4.6e+06;
Matches 12; Conservative 0; Mismatches 4; Indels
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Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Fax: 00497071601371
   Std Error: 0.00
Insert Length: 10000 Std Error: 0 Plate: 0319 row: H column: 15 Seg primer: CACACAGGAAACAGGTATGACC Class: plasmid ends High quality sequence stop: 20. Location/Qualifiers
                                                                                                                                                                                                                            'organism="Mus musculus"
                                                                                                                                                                                                                                                      /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:10090"
/clone="UUGC1M0319H15"
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Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.

(CE 1 (bases 1 to 20)

RS Dun, D., Aoyad; A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center
University of Utah Genome Center
University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwall [4]4732114[5]AP1A29072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XII0-Gold (Stratagene) cells and selected for ampicillin resistance."
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1M0319H15R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
                                                                                                                                                                                                                                                                                                                                                                                                              /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-" /clone_lib="Mouse_10kb plasmid UTGCIM library" /note="Vector: PWD42Lv; Purified genomic DNA from M.musculus C57BL/6J (male) was obtained from the Jackson
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46.7%; Score 9.8; DB 8; Length 19;
Best Local Similarity 84.6%; Pred. No. 3.6e+06;
Matches 11; Conservative 0; Mismatches 2; Indels
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            Std Error: 0.00
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Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ende
High quality sequence stop: 19.
Location/Qualifiers
                                                                                                                                                                                                                     /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="UUGC2M0190A02"
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AZ308384 1085 29-SEP-2000 1M0011K17F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0011K17 F, genomic survey sequence.
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Unpublished (2000)

Unpublished (2000)

University of Utah Genome Center
University of Utah Genome Center
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Sciurognathi, Muridae; Murinae, Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rm. 308, Biomedical Polymers. Research Bldg., 20 S. 2030 B., SLC,
84112, USA
                                                                                                                    /db_xref="taxon:54126"
/clone lib="mixed stage fosmid library of P. pacificus
var. California
/note="Vector: pEpifos-5 Fosmid vector"
                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                               Score 9.4; DB 9; Length 17;
Pred. No. 5.7e+06;
0; Mismatches 1; Indels
                                  1. 17
forganism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="california"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: 801 585 5606

Pax: 801 585 7177

Email: ddunm@genetics.utah.edu

Insert Length: 10000 .Std Error: 0.00

Plate: 0011 row: K column: 17

Seq primer: CGTTGTAAAACGACGGCCAGT
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/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             High quality sequence stop: 20.
Location/Qualifiers
                   Location/Qualifiers
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Best Local Similarity 90...
Best Local 10, Conservative
fosmid ends
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                     FEATURES
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AP129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (Basea I to 20)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse, Whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AZ316351 10008 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0034A11 F, genomic survey sequence.
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/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/lab host="E"
/clone lib="Mouse lokb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jacksou
Laboratory Mouse DNA Resource
Laboratory Mouse DNA Resource
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Fax: 801 585 7177
Email: dduun@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0034 row: A column: 11
Seq primer: CGTTGTAAAACGACGCCAGT
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/organism="Mus musculus"
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Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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Mus musculus
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ORIGIN

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Query Match
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                   10.5 Kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptore DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Wan 300, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
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Dunn,D., Aoyaqi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Relly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R., Mouse whole genome scaffolding with paired end reads from 10kb
adaptored DNA was purified and size-selected for a 9.5 to
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/clone_lib="Mouse_lokb plasmid UTGCIM library"
/note="Vector: PWD42rv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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Pred. No. 7.4e+06;
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0052 row: A column: 01
Seg primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
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/organism="Mus musculus"
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/clone="UUGC1M0052A01"
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                       cn 43.8%;
1 Similarity 78.6%;
11; Conservative
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Best Local Similarity
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AUTHORS
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COMMENT

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Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Evry cedex, FRANCE
Caston Cremieux, 91057 Evry cedex, FRANCE
PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at http://dbsgap.versailles.inra.fr/publiclines/. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).
                         electrophoresis. Vector DNA was prepared from a derivative of pND42 (gi[4732114]qb]AR12907211), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into adaptore becomplement B. coli X110-Gold (Stratagene) cells and selected for ampicillin resistance."
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T-DNA integration into the Arabidopsis genome depends on sequences
adaptored DNA was purified and size-selected for a 9.5 to
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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0
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     43.8%; Score 9.2; DB 8; Length 20
1 Similarity 78.6%; Pred. No. 7.4e+06;
11; Conservative 0; Mismatches 3; Indels
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GSS; left border; T-DNA flanking sequence.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Arabidopsis thaliana"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol type="genomic DNA"
/cultivar="Wassillewskija"
/db xref="taxon:3702"
/clone="275G07"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of pre-insertion sites
EMBO Rep. 3 (12), 1152-1157 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                left border"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 GCGTATCTGAAGAG 17
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Balzergue, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
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Best Local Similarity
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DEFINITION

RESULT 12

ઠ 셤 AJ684587

ORGANISM ACCESSION VERSION KEYWORDS SOURCE

REFERENCE AUTHORS TITLE

JOURNAL

COMMENT

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/gas="Male"
//lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
//clon=lib="Mouse loke plasmid UUGCIM library"
//clon=lib="Mouse loke plasmid UUGCIM library"
//note="Vector: PWMSIAN; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymuclectide kinase. Adaptor oligonuclectides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMAP2 (gil 4732114[gb]AP129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was ennealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
                                                                                                                                                                                                                                    Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BG924548 1inear EST 06-NOV-2001
HNC27-1-G10.R HNC (Human Normal Cartilage) Homo sapiens CDNA, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. It (bases I to 21). Kumar, S., Connor, J.R., Dodds, R.A., Halsey, W., Van Horn, M., Mao, J., Sathe, G., Mui, P., Agarwal, P., Badger, A.M., Lee, J.C., Gowen, M. and
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss R. Wouse whole genome scaffolding with paired end reads from 10kb plasmid inserts Unpublished (2000) Contact Robert B. Weiss University of Utah Genome Center University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ch 42.9%; Score 9; DB 8; Length 20; 1 Similarity 70.6%; Pred. No. 9.3e+06; 12; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                   Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Brror: 0.00
Plate: 0465 row: C column: 08
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C578L/63"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:10090"
/clone="UUGC1M0465C08"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         High quality sequence stop: 20.
Location/Qualifiers
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BG924548.1 GI:14319071
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Homo sapiens
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Best Local Similarity
Matches 12; Conserv
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LOCUS
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AUTHORS
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KEYWORDS
SOURCE
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                                                                                                                                    JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURES
                                                                           TITLE
                                                                                                                                                            COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anderson, S. I., Finlayson, H.A. and Archibald, A. L.
Development of CDNA and EST resources for studying reproduction and
embryo development in pigs and cattle
Unpublished (2004)
Contact: Anderson SI
Genomics and Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Stoplin, Midlothian, EH25 9PS, UNITED KINGDOM Single pass sequencing. Bases called and trimmed with phred v0.020425.c. Vector identified by cross match with the -minscore 20 and -minmatch 12 options. Vector:pBlueScriptII (KS+) R. Sitel: EcoRI R. Sitel: NotI 5' Seq Primer M13F Normalised library constructed from pig uterus. Clones available from UK Centre for Functional Genomics in Parm Animals, Roslin Institite, Roslin, Midlothian, UK, EH25 9PS, www.arkgenomics.org.
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AZ625776
                                                                                                                                                                                                                                                                                                         AJ684587 CSEQRAN04 Sus scrofa cDNA clone C0001805_G15, mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (Dases 1 to 20)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Cetartiodactyla, Suina, Suidae, Sus.
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                                                   Gaps
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                                                Indels
                  Pred. No. 8.5e+06; 
; Mismatches 0;
                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Sus scrofa"
/mol_type="mXNA"
/db_xrefe"taxon:9823"
/clone="C0001805_G15"
/tissue_type="uterus"
/clone_lib="CSEQRAN04"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (house mouse)
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                  100.08;
                  Best Local Similarity 100.
Matches 9; Conservative
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Best Local Similarity 100.
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sus scrofa (pig)
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                                                                                                         13 AAGAGTCTG 21
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                                                                                                                                                                                                                                                                                                                                                                        sequence.
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source

DRIGIN

FEATURES

DEFINITION

ACCESSION VERSION KEYWORDS SOURCE

RESULT 13 AZ625776

ઠે 셤 ORGANISM

REFERENCE AUTHORS

Gapa

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C00979 20 bp mRNA linear EST 31-DEC-2002
HUMGS0003365 Human adult (K.Okubo) Homo sapiens cDNA, mRNA
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 20)
                                                       /organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/cultivar="Wassillewskija"
/db_xref="taxon:3702"
/clone="233H03"
/clone="233H03"
/ clone=lb="Arabidopsis thaliana T-DNA insertion lines"
/note="T-DNA flanking sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1-3, Yanada-oka, Suita, Osaka Pref. 565, Japan
Tel: 06-877-5111(ex.3115)
Tel: 06-877-5111(ex.3115)
Tel: 06-877-5111(ex.3115)
Tel: 06-877-5111(ex.3115)
We are not submitting the same cDNA sequence redundantly to DDBJ since 1993. For the abundance information of clones with this since 1993. For the abundance information of clones with this libraries, see 'http://www.imcb.osaka- u.ac.jp/bodymap'. The sequences of the clones represented by this GS sequences is also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (K.Okubo) "
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Pred. No. 1.2e+07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Okubo, K.
Institute for Molecular and Cellular Biol
                                                                                                                                                                                                                                                                                                            Score 8.8; DB 9;
Pred. No. 1.1e+07;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BodyMap, human gene expression database Unpublished (1995)
http://genoplante-info.infobiogen.fr/
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
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/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          db_xref="taxon:9606"
|dev_stage="adult"
|clone_lib="Human adult
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20 bp
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.1 Similarity 83.3%;
10; Conservative (
                                                                                                                                                                                                                                                                                                               41.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C00979.1 GI:1433209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (human)
                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 83.3
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 ATCTGAAGAGTC 19
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12 CGTAGTTGAAGA 1
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Best Local Similarity
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Direct Submission

Direct Submission

Submitted (13-007-2003) Balzergue S., UWRGV, INRA/CNRS, 2 rue

Gaston Cremieux, 91057 Evry cedex, FRANCE

PCR was performed on DNA from transformants of Arabidopsis thaliana

plants from INRA (Versailles). The DNA fragment(s) resulting from

the PCR were directly sequence from the left or the right border

to determine the genomic sequence flanking the insertion. T-DNA

derived sequences were removed. Information to order the

corresponding muteant line and a link to a database providing a

graphical display of the insertion site are available at

http://dbsgap.versailles.inra.fr/publiclines/. This sequence has

been generated in the framework of the French plant genomics

program 'Genoplante' (http://www.genoplante.com and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AJ587168 17 bp DNA linear GSS 15-JAN-2004
Arabidopsis thaliana T-DNA flanking sequence, left border, clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Brunaud, V., Balzergue, S., Dubreucq, B., Aubourg, S., Samson, F., Ahauvin, S., Bechtold, N., Cruaud, C., DeRose, R., Pelletier, G., Lepiniec, L., Caboche, M. and Lecharny, A.
T-DNA integration into the Arabidopsis genome depends on sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                     Contact: Sanjay Kumar
UW2109
GlaxoSmithKline
709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
Tel: 610-270-7245
  Lark,M.W.
Identification and initial characterization of 5000 expressed sequenced taggs (EST9) each from adult human normal and osteoarthritic cartilage cDNA libraries
Osteoarthr. Cartil. 9 (7), 641-653 (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="mRNA"
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/tissue_type="cartilage"
/tissue_type="cartilage"
/clone_lib="HNC (Human Normal Cartilage)"
/note="Vector: pSPORT I; Site_1: SalI; Site_2: NotI;
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GSS; left border; T-DNA flanking sequence.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
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Matches 9; Conservative 0; Mismatches
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EMBO Rep. 3 (12), 1152-1157 (2002)
22363535
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/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    genomic survey sequence.
                                                                                                                                                                                                                                                                        Fax: 610-270-5598
Email: sanjay_kumar-1@gsk.com
Seq primer: T7.
                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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Gaps

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Contact: Anderson SI
Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred
Single pass sequencing. Bases called and trimmed with the -minscore 20
v0.02045.c. Vector identified by cross_match with the -minscore 20
and -minmatch 12 options. Vector: pBluescriptis(8k+) R. Site 1:
ECORI R. Site 2: NotI 5' Seq primer M13F Description: Normalised
library constructed from Bovine Uterus tissue. Clones available
from UK Centre for Functional Genomics in Farm Animals, Roslin
Institite, Roslin, Midlothian, UK, EH25 9PS, www.arkgenomics.org.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 19)
Anderson, S.I., Finlayson, H.A. and Archibald, A.L.
Development of cDNA and EST resources for studying reproduction and
embryo development in pigs and cattle
Unpublished (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AJ671616
AJ671616 KN224 Bos taurus CDNA clone KN224-006_N20, mRNA sequence.
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                                                                                                                                                                                                                                                        /clone lib="Human promyelocyte"
/note="Pemale, adult, cell_line = HL60, cell_type =
promyelocyte. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41.0%; Score 8.6; DB 1; Length 19; 73.3%; Pred. No. 1.5e+07; ive 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
41.9%; Score 8.8; DB 7; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.2e+07;
Matches 10; Conservative 0; Mismatches 2; Indels
Osaka University
3-1 Yamada-oka,Suita,Osaka 565,Japan.
Location/Qualifiers
                                                                                                                          /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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/organism="Bos taurus"
/mol_type="mtWN4"
/db_xref="taxon:9913"
/clone="KN224-006_N20"
/tissue_type="uterus"
/clone_lib="KN224"
                                                                                                                                                                                                                                 /clone="pm2147"
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AJ671616.1 GI:49356473
EST.
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AJ671616/c
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                                                                                                                                                                                            Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
Enthartoideae; 
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1 (bases 1 to 20)
Okubo, K., Pukushima, A., Yoshii, J., Nilyama, T., Kojima, Y.,
Yoshinari, H., Arimotto, J. and Matsubara, K.
Gene expression of human promyelocytic cell line HL60 before and after induction of differentiation. A new application of 3'directed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /dev stage="14 days after germination"
/lab_host="E.coli SOLR"
/lab_host="E.coli SOLR"
/clone_libe="AtJOH--Overexpressing transgenic rice lambda
phage cDNA libeary (JWT1)"
/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
XhoI; cDNA was inserted into lamda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site. mRNA was
prepared from Arabidopsis Jasmoinate Carboxyl
methyltransferase overexpression line."
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Institute for Molecular and Cellular Biology
      JMT1--03-A01.gl AtJMT-overexpressing transgenic rice lambda phage clobA library (JMT1) Oryza sativa (japonica cultivar-group) cDNA clone JMT1--03-A01, mRNA sequence.
CF32351
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HUMGS01685 Human promyelocyte Homo sapiens cDNA clone pm2147 3'
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    .20
/organism="Oryza sativa (japonica cultivar-group)"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:39947"
/clone="JMT1--03-A01"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
/cultivar="Nackdong"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tissue_type="leaf"
                                                                                                                                           CF325351.1 GI:33798984
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Unpublished (1993)
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41.9
Best Local Similarity 83.3
Matches 10; Conservative
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Gaps

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Imboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/duares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pwD42 (gi|4732114|gb|AR129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adappored vector DNA, and transformed into
chemically-competent E. coli XII0-Gold (Stratagene) cells
and selected for ampicillin resistance."
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammala; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts
                                                                                                              20 S. 2030 E., SLC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /sex="Male"
/lab host="B. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42rry; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                   Rm. 308, Biomedical Polymers Research Bldg., 84112, USA
                                                                                                                                                          Tel: 801 585 5606
Fax: 801 585 7177
Fax: 801 585 7177
Fax: 802 585 7177
Fax: 803 587 7177
Fax: 803 587 7177
Fax: 803 row: D column: 18
Seq primer: CGTGTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 20.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Mus musculus"
                 Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:10090"
/clone="UUGC1M0302D18"
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Unpublished (2000)
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AZ658035/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Ambystoma mexicanum"
/mol_type="maNA"
/db_zref="taxon:8296"
/tisque_type="radii Blastema"
/cell_type="regenerating tail blastema"
/clone_libe="c-bay Axolot| Tail Blastema"
/clone_libe="c-bay Axolot| Tail Blastema" (6DAxBL)"
/note="Vector: pCWNSport6; Site 1: Not1; Site 2: Sall;
/normalized cDNA plasmid library prepared by_Invitrogen.
Size fractionated mNNA was polydf primed and cloned into
Not1-Sall site of pCWNSport6. Bacterial host is
EMDHIOB-TONA. Average insert size is 1.67 kB.
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                          CO778852 19 bp mRNA linear EST 05-AUG-2004
BLO04D_H08 6-Day Axolotl Tail Blastema (6DAXBL) Ambystoma mexicanum
CDNA 5' similar to hypothetical protein, mRNA sequence.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bummalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)
                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Caudata, Salamandroidea, Ambystomatidae,
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41.0%; Score 8.6; DB 7; Length 19;
Best Local Similarity 73.3%; Pred. No. 1.5e+07;
Matches 11; Conservative 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: 0049 351 210 2620
Fax: 0049 351 210 1489
Email: tanaka@mji-cbq.de
Plate: BL004D row: 08 column: H
Seq primer: GCA CAT TAG GCC TAT TTA GGT GAC A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfotenhauerstrasse 108,01307 Dresden, Germany
                                                                                                                                                                                                   Ambystoma mexicanum (axolot1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genome Biol. (2004) In press
Contact: Elly M. Tanaka
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Hoon, S.T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H. Direct Submission
Submitted (07-JAN-2002) Hong-Seog Park, Korea Research Institute of Bioscience and Biotechnology (KRIBB), Genome Research Center (GRC); S.2, Oun-dong, Yusong-gu, Daejeon 305-333, Korea
(E-mail:redstone@mail.kribb.re.kr, URL:http://phs.grc.kribb.re.kr/, Tel:82-42-866-7181, Fax:82-42-860-4409)
Clones are derived from the chimpanzee BAC library RP-43 This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.
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84112, USA
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1M0461M13F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0461M13 F, genomic survey sequence.
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Dunn, D., Aoyaqi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Niederhausern, A., and Wright, D., Weise, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weise, R., Mouse, whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cell type="lymphocytes"
clone_lib="RP-43 Chimpanzee Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41.0%; Score 8.6; DB 9; Length 21; 73.3%; Pred. No. 1.5e+07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="RP43-072L24.T7"
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Seg primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
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Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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Fax: 801 585 7177
Email: ddunmgenetics.utah.edu
Insert Length: 10000 Std Brro:
Plate: 0461 row: M column: 13
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Mus musculus
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Best Local Similarity 73.3
Matches 11; Conservative
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                               Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
TRM. 308, Biomedical Polymers Research Bldg., 20 S. 2030 B., SLC, UT
84112, USA
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Pan troglodytes DNA, clone: RP43-072L24.T7, genomic survey
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Pan.
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/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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                                                                                                                                                             Tel: 801 585 5606
Pax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0534 row: P column: 03
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                     organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="UUGC1M0534P03"
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/sex="Male"
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                                                          /lab_host="E. Coli strain XLIO-Gold, Tl-resistant, F-"
/clone_lib="Mouse_lokb plasmid UTGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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Insert Length: 10000 Std Error: 0.00
Plate: 0088 row: M column: 08
Seg primer: CGTTCTAAAACGACGCCAGT
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/mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="UUGC1M0461M13"
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Fax: 801 585 7177
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/gex="Male"
// Jab hose="E. Coli strain XLIO-Gold, Tl-resistant, F-"
// Clone lib="Wouse 10kb plasmid UUGCIM library"
// Clone lib="Wouse 10kb plasmid UUGCIM library"
// Clone lib="Wouse 10kb plasmid UUGCIM library"
// Mouse DRA Resource
// Mouse DRA Resource
// Choose library 
                                                            AZ787920 21 bp DNA linear GSS 16-FBB-2001 2M0034M09R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC2M0034M09 R, genomic survey sequence.
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Unpublished (2000)
Contact: Nobert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 B., SLC,
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
lnsert Length: 10000 Std Error: 0.00
Plate: 0034 row: M column: 09
Seq primer: CACACAGGAAACAGCTAATGACC
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/organism="Mus musculus"
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/strain="C578L/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0034M09"
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Submitted (07-JAN-2002) Hong-Seog Park, Korea Research Institute of Bioscience and Biotechnology (KRIBB), Genome Research Center (GRC); S., Oun-dong, Yusong-gu, Daejeon 305-333, Korea
(B-mail:redstone@mail:kribb.re.kr, URL:http://phs.grc.kribb.re.kr/, Tel:82-42-866-7181, Fax:82-42-860-4409)
Clones are derived from the chimpanzee BAC library RP-43 This BAC Clones are derived from the chimpanzee BAC library RP-43 This BAC
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Pan troglodytes DNA, clone: RP43-088M10.TJ, genomic survey
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Pan.
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/clone_lib="RP-43 Chimpanzee Male BAC Library"
                                                                                                                                                                                          cell type="lymphocytes"
/clone_lib="RP-43 Chimpanzee Male BAC Library"
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/clone="RP43-088M10,TJ"
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Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred
Single pass sequencing. Bases called and trimmed with the -minscore 20
and -minmatch 12 options. Vector:pBlueScriptII(KS+) R. Site 1:
EGGR R. Site 2: NotI Description: Normalised library constructed
from pooled tissue from day 30 placentas. Clones available from W
Centre for Functional Genomics in Farm Animals, Roslin Institute,
Roslin, Midlothian, UK, EH25 9PS, www.arkgenomics.org.
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1 (bases 1 to 18)
Anderson, S.I., Finlayson, H.A. and Archibald, A.L.
Development of cDNA and EST resources for studying reproduction and Unpublished (2004)
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/clone="C0000023 015"
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/clone lib="CSEQRAN09"
/note="Vector: pBlueScriptII(KS+); Site_1: EcoRI; Site_2:
Not1; Single pass sequencing. Normalised library
constructed from pooled tissue from day 30 placentas."
Sequence Sequence flanking probable Mu insertion site in UniformMu line: 0180557-03, Primer set: A Class: transposon insertion site.
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Pred. No. 2.3e+07;
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                                                                                                   Location/Qualifiers
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76.9%;
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Matches 10; Conserv
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                                                                         CL694050 13 bp DNA linear GSS 10-JUL-2004 PRI0163a H11_2 - PRI0163a.BR (13) Mixed stage fosmid library of P. pacificus var. California Pristionchus pacificus genomic, genomic
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoldeae, Andropogoneae, Zea.
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01S0557-03A1-C12 UniformMu MuTAIL Library Zea mays genomic clone
01S0557-03A1-C12, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone lib="Mixed stage fosmid library of P. pacificus var. California" /note="Vector: pEpifos-5 Fosmid vector"
                                                                                                                                                                                                                                                                                  Pristionchus pacificus
Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
1 (Dasses 1 to 13)
Srinivasan, J., Otto, G. W., Kahlow, U., Geisler, R. and Sommer, R.J. AppadB: an AcedB database for the nematode satellite organism
Pristionchus pacificus
Nucleic Acids Res. 32 (1), D421-D422 (2004)
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Latshaw,S., Tan,B-.C., Settles,A.M. and McCarty,D.R.
Sequence tagged transposon insertions from the UniformMu maize
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fax: 00497071601498
Email: ralf: commer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
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Pred, No. 2.2e+07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
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Contact: Donald R. McCarty
Contact: Donald R. McCarty
University of Florida
PO 110690 Gainesville, FL 32611-0690, USA
Email: 352-392-1928 x322
Email: drm@ufl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
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Class: fosmid ends.
Location/Qualifiers
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CL423467
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TITLE
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AJ588865 LOCUS

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(http://www.jax.org/resources/documents/dhares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end with T4 DNA polymerase and T4 polymuclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pubAl (gil-#1732114|gb]AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xili0-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                     Mus musculus (house mouse)

Mus musculus

Bukartyota; Matazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Musmania; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Musmania; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 19)

S Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Menen, E., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /sex="Male" /lab host="B. Coli strain XL10-Gold, T1-resistant, F-" /lab host="B. Coli strain XL10-Gold, T1-resistant, F-" /clone lib="Mouse 10kb plasmid UUGCIM library" /note="Wetcr: PWD42nr; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39.0%; Score 8.2; DB 8; Length 19; 76.9%; Pred. No. 2.38+07; arive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0101 row: K column: 12
Seg primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Laboratory Mouse DNA Resource
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/strain="C57BL/6J"
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Location/Qualifiers
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/clone="UUGC1M0101K12"
AZ358656.1 GI:10472356
GSS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: 801 585 5606
Fax: 801 585 7177
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Submitted (23-OCT-2003) Balzerque S., UMRGV, INRA/CNRS, 2 rue
Gaston Cremieux, 91057 Evry cedex, FRANCE
FCR was performed on DNA from transformants of Arabidopsis thaliana
plants from INRA (Versailles). The DNA fragment(s) resulting from
the PCR were directly sequenced from the left or the right border
to determine the genomic sequence flanking the insertion. T-DNA
derived sequences were removed. Information to order the
corresponding mutant line and a link to a database providing a
graphical display of the insertion site are available at
http://dbsgap.versailles.inra.fr/publiclines/. This sequence has
program Generated in the framework of the French plant genomics
program Genoplante' (http://www.genoplante.com and
http://genoplante-info.infobiogen.fr).
Location/Qualifiers
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                                                                                                                                                                                                                                                                           AJ588865 18-JAN-2004 Arabidopsis thaliana T-DNA flanking sequence, right border, clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Brunaud, V., Balzergue, S., Dubreucq, B., Aubourg, S., Samson, F., Chauvin, S., Bechtold, N., Cruaud, C., DeRose, R., Pelletier, G., Lepiniec, L., Caboche, M. and Lecharny, A.

T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites

of pre-insertion sites

ERROR Rep. 3 (12), 1152-1157 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AZJSB656 19 bp DNA linear GSS 02-OCT-200 1M0101K12F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0101K12 F, genomic survey sequence. AZJSB656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
            Gaps
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            3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                      AJ588865.1 GI:37938489
GSS, right border; T-DNA flanking sequence.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Arabidopsis thaliana"
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/cultivar="Wassillewskija"
/db_xref="taxon:3702"
/clone="539G02"
            Mismatches
                                                                                                                                                                                                                                                                                                                                             539G02, genomic survey sequence.
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Balzergue, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8 ATCTGAAGAGTCT 20
                                                                        3 GGCGTATCTGAAG 15
                                                                                                                                2 GGCGTCTTTGGAG 14
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               10; Conservative
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Matches 10; Conserv
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AZ358656/c
LOCUS
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Gaps .. 0

DEFINITION

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ACCESSION

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/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/clone lib="Wouse 10kb plasmid UUGCIM library"
/mote="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end repaired with T4 DNA polymerses and T4
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse annealed to
                                                                                                                   Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
University of Utah
84112, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I bases 1 to 20.
Dunn, D., Aoyaqi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
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Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                      Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                         Plate: 0040 row: D column: 05
Seq primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="genomic DNA"
/strain="C578L/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:10090"
/clone="UUGC1M0040D05"
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Best Local Similarity 76.9%;
Matches 10; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sex="Male"
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                                                                                                                                                                                                                                                                                               Tel: 801 585 5606
Fax: 801 585 7177
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AZ436082
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KEYWORDS
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                                                                  TITLE
                                                                                                                                                    COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="MPIZ-ADIS-024-developing root"
/note="Vector: pCMVSPORT6; Site_l: Sal1; Site_2: Not1;
cDNA library from sugar bett, library provided by KWS
Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sal1-Not1, primer sites and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20 bp DNA linear GSS 29-SEP-2000 smid UUGCIM library Mus musculus genomic
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                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Gapernatophyta; Garyophyta; Caryophyllales; Amaranthaceae; Beta.

1 (base 1 to 20)

1 (base 1 to 20)

1 (base 1 to 20)

2 (base 1 to 20)

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4 (base 1 to 20)

5 (base 1 to 20)

6 (base 1 to 20)

7 (base 1 to 20)

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8 (base 1 to 20)

9 (base 1 to 20)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SP6-SAIL-CCACGCGTCCG-Sprime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"
                                                                                                                                                                                                                                                                                                                                                                                                                                                          1
                                                                                                                                                                                                                                                                                                                              Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes Plant J. 32 (5), 845-857 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 8.2; DB 5; Length 20; Pred. No. 2.3e+07; 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Weisshaar B
ADIS DNA core facility at MPIZ
MAX-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1M0040D05F Mouse 10kb plasmid UUGC1M library Muclone UUGC1M0040D05 F, genomic survey sequence. AZ320114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: weisshaa@mpiz-koeln.mpg.de
Insert Length: 20 Std Error: 0.00
Plate: 22 row: L column: 12
Seg primer: SP6; CATACGATTARGGTGACACTATAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="developing root"
/lab_host="EMDH10B"

    .20
    /organism="Beta vulgaris"

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/clone="024-022-L12"
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            3Q595520.1 GI:26125103
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76.9%;
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                                                                     Beta vulgaris
                                                                                                   Beta vulgaris
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PUBMED
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AZ320114
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High quality sequence stop: 2
Location/Qualifiers
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Mus musculus (house mouse)
Mus musculus
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Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                Rm. 308, Bi
84112, USA
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AZ807038
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                                                                                 Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Winversity of Utah
Win 308, Biomedical Polymers Research Bldg., 20 S. 2030 B., SLC, UT
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 20)

Dunn,D., Aoyaqi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
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20 bp DNA linear GSS 16-FEB-200
1M0583M24R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
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/clone lib="Mouse 10kb plasmid UGCIM library"
/note="Twetcor: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
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                                                                                                                                                                                                                                                                         Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0233 row: A column: 10
Seq primer: CACACAGGAAACAGCTATGACC
Class: plaemid ends
High quality sequence stop: 20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:10090"
/clone="UUGC1M0233A10"
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AZ772787.1 GI:12896465
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1 Similarity 76.9%;
10; Conservative (
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Fax: 801 585 7177
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunc norifice at constant velocity. The sheared DNA was blunc end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gal electrophoresis. Vector DNA was prepared from a derivative of pMAQ2 (gql/4732114(gbl/AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Killo-Gold (stratagene) cells and selected for ampicillin resistance."
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /sex="Male"
/lab host="B. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                              Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.(
Plate: 0583 row: M column: 24
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Mus musculus"
                                                                                                              plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0583M24"
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JOURNAL

COMMENT

TITLE

FEATURES

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Email: hicksgg@cc.umanitoba.ca
U3NeoSV1 gene trap. Tag generated by plasmid rescue. Additional
sequence information and target gene cloning can be generated. ES
cell line harboring insertion mutation of target gene is available.
                                                                                                                                                                                                                                                                                                   Sequence analysis available from http://140.193.242.7/esdb/public_search_frame.php?PST=PST3869-NR.Se
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HNC1-1-G11.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA
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Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J.,
Sathe,G., Mui,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Identification and initial characterization of 5000 expressed sequenced tags (ESTs) each from adult human normal and osteoarthritic cartilage cDNA libraries Osteoarthr. Cartil. 9 (7), 641-653 (2001)
Unpublished (2002)
Contact: Hicks GG
Mammalian Functional Genomics Centre
Manitoba Institute of Cell Biology, Universitry of Manitoba
ON5029, 675 McDermot Ave, Winnipeg, MB R3E 0V9, Canada
Fax: 204 787 2190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /sex="Male"
/cell type="Embryonic stem cell"
/cell line="D3H (J1 subclone)"
/clone lih="MICB1"
/note="Vector: U3NeoSV1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ch 39.0%; Score 8.2; DB 9; 1 Similarity 61.9%; Pred. No. 2.3e+07; 13; Conservative 0; Mismatches 8;
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                               organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="genomic DNA"
/strain="129 sv"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="PST3869-NR.Seg"
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Fax: 610-270-5598
Email: sanjay_kumar-1@gsk.com
Seg primer: T7.
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Class: Gene Trap.
Location/Qualifiers
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UW2109
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Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (http://www.jax.org/resources/documents/dhares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gi|q192114|gpl|APL29072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the innert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 21)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus G57846 (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
                                                                                                                  Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Wm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, 84112, USA
             Reilly, M., Rose, M., Rose, R.; Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
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                                                                                                                                                                                                                                                                                                                              Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Brror: 0.00
Plate: 0069 row: C column: 06
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:10090"
/clone="UUGC2M0069C06"
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GSS.
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Best Local Similarity 76.9
Matches 10; Conservative
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Fax: 801 585 7177
                                                                                               plasmid inserts
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DEFINITION

LOCUS

ACCESSION

RESULT 39 CL436802

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ORIGIN

REFERENCE AUTHORS TITLE

; 0

Gaps

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/tissue type="cartilage"
/lab_host="E.coli DH10 B"
/clone_lib="HNC (Human Normal Cartilage)"
/note="Vector: pSPORT 1; Site_1: Sal1; Site_2: Not1;
Directional"
                                                                                                                                                                                       Query Match 38.1%; Score 8; DB 4; Length 11; Best Local Similarity 100.0%; Pred. No. 2.7e+07; Matches 8; Conservative 0; Mismatches 0; Indels
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0; Gaps

1 CTGGCGTA 8 |||||||| 9 CTGGCGTA 2 ò g Search completed: August 12, 2005, 11:03:27 Job time : 1812 secs

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AX130020 Sequent AX130021 Sequent AX269412 Sequent AX270943 Sequent AX270943 Sequent AX378663 Sequent AX378663 Sequent AX1733092 Sequent CQ770343 Sequent CQ770343 Sequent	AR312207 Sequence AR359611 Sequence AR259854 Sequence AX259854 Sequence AX259855 Sequence BD254799 Regulatio BD254800 Regulatio BD254801 Regulatio AX10664 Sequence AR567503 Sequence AR577553 Sequence	AXA18117 Sequence AXB1290 Sequence E30865 Oligonucleo E37662 Method for I58336 Sequence AXB0675 Sequence AXB0675 Sequence AX693269 Sequence AX693270 Sequence AX693271 Sequence AX759814 Sequence AX759814 Sequence AX759814 Sequence AX759814 Sequence AX759815 Sequence AX769817 Sequence AX769817 Sequence AX769818 Sequence AX769818 Sequence AX769818 Sequence AX769818 Sequence AX769818 Sequence AX769818 Sequence AX26904 Sequence AX26904 Sequence AX26904 Sequence	BD009147 Herbicide BD067559 Enzymatic CQ786886 Sequence CQ786886 Sequence AR108117 Sequence AR108171 Sequence AR108171 Sequence AR10817 Sequence AR10817 Sequence AR10817 Sequence AR1082051 Sequence B26923 Vascular en AR206672 Sequence AR097061 Sequence AR097061 Sequence BD231398 Isolated BD231398 Isolated E3620 Japanese ci E3620 Japanese ci E47018 Simulataneo AR20163 Sequence AR25968 Sequence AR297463 Sequence AR297463 Sequence AR297463 Sequence AR297463 Sequence AR297463 Sequence AR297463 Sequence AR29763 Sequence AR29763 Sequence AR36995 Sequence AR136995 Sequence AR459958 Sequence AR459958 Sequence	AX673751 Sequence
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11.4 57. 111.4 57. 111.2 56. 111.2 56. 111.2 56. 111.2 56.	11.2 56. 11.2 56. 11.2 56. 11.2 56. 11.2 56. 11.1 55.	10.0 8 8 5 4 4 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	64 10.6 53.0 65 10.6 53.0 69 10.6 53.0 69 10.6 53.0 72 10.6 53.0 73 10.6 53.0 73 10.6 53.0 74 10.6 53.0 75 10.6 53.0 76 10.6 53.0 77 10.6 53.0 88 10.6 53.0 88 10.6 53.0 89 10.6 53.0 89 10.6 53.0 89 10.6 53.0 80 10.6 53.0 81 10.6 53.0 82 10.6 53.0 83 10.6 53.0 84 10.6 53.0 85 10.6 53.0 86 10.6 53.0	10.4 52.
c c conds c			a inted, n equence	ance C
n 5.1.6 Compugen Ltd. Search time 1581 Seconds (without alignments) 612.969 Million cell upda	0.000		predicted by chance to have a socre of the result being printed, total score distribution. ARIES Description AR312275 Sequence BD217452 Antisense AR031072 Sequence BD317452 Antisense AR031072 Sequence BD3134289 Detection AX75344 Sequence BD134289 Detection AX75906 Sequence A65727 Sequence BA65727 Sequence BA65727 Sequence BA65727 Sequence BA65727 Sequence BA65727 Sequence A65727 Sequence A65727 Sequence BA65727 Sequence BA65727 Sequence BA65727 Sequence BA65727 Sequence BA65727 Sequence AX353519 Sequence AX353519 Sequence BA65727 Sequence AX3670708 Sequence BA7636229 Sequence BA7636229 Sequence BA7636229 Sequence BA7636229 Sequence BA7636229 Sequence BA763644 Sequence BA764674 Sequence	AK364674 Seque AX734698 Seque

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E 1 (Dases 1 to 18)

Shaker, B.F. and Cowsert, L.M.
Antisenses modulation of TNFR1 expression
Antisenses modulation of TNFR1 expression
Datent: JP 2002519015-A 75 02-JUL-2002;
ISIS PHARMACEUTICALS INC
OS Unidentified
PN JP 2002519015-A/75
PD 02-JUL-2002
PF 17-JUN-1999 JP 2000557265
PR 26-JUN-1999 US 09/106038
PR 26-JUN-1999 US 09/106038
PR PRENDA F BAKER, LEX M COWSERT
PC 12015/09, A61K31/7105, A61K31/711, A61K48/00, A61P29/00, A61P43/00, PC
               PAT 17-JUL-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 20)
Polymeropoulos, M.H. and Merril, C.R.
Bleven highly informative microsatelite repeat polymorphic DNA markers
Patent: US 5861504-A 60 19-JAN-1999;
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                 linear
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Topology: Linear;
Antisense modulation of TNFR1 expression
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Location/Qualifiers
       18 bp DNA
Antisense modulation of TNFR1 expression.
BD217452
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                                                          BD217452.1 GI:33027222
JP 2002519015-A/75.
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AR031072.1 GI:5944286
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unclassified.
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PC C12N1!
CC Stranc
CC Topolc
CC Antisc
FH Key
FT sourc
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                                                                                                                                                                                                                                                                                                            Unknown.
Unclassified.
Unclassified.
Unclassified.
I bases I to 20)
Griffals,R., Hoiseth,S.K., Zagursky,R.J., Metcalf,B.J., Peek,J.A., Sankaran,B. and Fletcher,L.D.
Chlamydia pneumoniae polynucleotides and uses thereof
Patent: US 6559294-A 2012 06-MAY-2003;
Location/Qualifiers
AX693266 Sequence
AX75398 Sequence
AX73386 Sequence
AX745403 Sequence
AX745404 Sequence
AX745405 Sequence
AX745406 Sequence
AX745406 Sequence
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Baker, B.F. and Cowsert, L.M.
Antisense inhibition of TNFR1 expression
Patent: US 6007995-A 75 28-DEC-1999;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA
                                                                                                                                                                                                                            AR312275 20 bp DN.
Sequence 2812 from patent US 6559294.
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/mol_type="unassigned DNA"
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Sequence 75 from patent US 6007995.
AR096404
                                                                                                                                                      ALIGNMENTS
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/mol_type="genomic DNA"
 AX693266
AX725386
AX733563
AX745403
AX745404
AX745406
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AR312275
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                    Telerman, A., Amson, R. and Tuijnder, M.
Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or resistance to viruses and the use thereof as medicaments
Patent: WO 03025177-A 934 27-MAR-2003;
Molecular Engines Laboratories (FR)
Location/Qualifiers
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86.7%; Pred. No. 1.1e+05;
iive 0; Mismatches 2;
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Pred. No. 1.1e+05;
0; Mismatches 2;
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Sequence 2386 from Patent WO03040369.
AX759065
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Patent: WO 03040369-A 2386 15-WAY-2003;
Molecular Engines Laboratories (FR)
Location/Qualifiers
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                                        AX735344 17 bp DNA Sequence 934 from Patent WO03025177.
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                /mol_type="unassigned DNA"
/db_xref="taxon:9606"
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/organism="Homo sapiens"
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Sequence 8 from Patent WO9735973.
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                                                                         AX735344.1 GI:30514621
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Best Local Similarity 86.7%;
Matches 13; Conservative (
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Matches 13; Conservative
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Location/Qualifiers
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JP 2002505888-A/113.

Synthetic construct
synthetic construct
other sequences; artificial sequences.

(1 (bases 1 to 20)
Sidlandki, D.
Detection of neoplasia by analysis of saliva
Parent: JP 2002505888-A 113 26-FEB-2002;
PR JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
OS Artificial Sequence
N JP 2002505888-A/113
PD 26-FEB-2002
PF 10-MAR-1999 JP 2000535774
PR 10-MAR-1999 US 09/038637
PR 10-MAR-1998 US 09/038637
PR 10-MAR-1998 US 09/038637
PR 10-MAR-1998 US 09/038637
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Detection of neoplasia by analysis of saliva.
BD134289
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Sidransky, D.
Detection of neoplasia by analysis of saliva
Patent: US 6235470-A 113 22-MAY-2001;
Location/Qualifiers
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/organism="synthetic construct"
/mol type="genomic DNA"
/db_xref="taxon:32630"
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Seguence 113 from patent US 6235470.
ARIS2833
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/mol_type="unassigned DNA"
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GACCCCACAGCCTATTCAGA 20
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PAT 05-DEC-1998
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Momo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unknow...
Unclassified.
1 (bases 1 to 20)
Lacroix,J.-M. and Dunn,J.M.
Method and kit for quantitation and nucleic acid sequencing of nucleic acid analytes in a sample nucleic acidanalytes in a sample
Patent: US 579572-A 8 18-AUG-1998;
Location/Qualifiers
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Location/Qualifiers
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                                                          Artificial sequences.
JP 195285987-A/1
31-OCT-19585
SPAR-1994 JP 1994059386
KOMAI KOICHIRO, KANEKO HIDEO, NAKATSUKA IWAO
CO77421/44, C1201/68//C12N15/09;
trandedness: Single;
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86.7%; Pred. No. 1.1e+05;
tive 0; Mismatches 2;
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CYTOCHROME P45011C18
Patent: JP 1995285987-A 1 31-OCT-1995;
SUMITOMO CHEM CO LTD
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/organism="unknown"
/mol_type="unassigned DNA"
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AX207008
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    .18
    /organism="unidentified"
    /mol_type="genomic DNA"
    /db_xref="taxon:32644"

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Unclassified.

1 (bases 1 to 18)
1 (bases 1 to 18)
Komai,K., Kaneko,H. and Nakatsuka,I.
Komai,K., Kaneko,H. and Nakatsuka,I.
Oligonucleotide for use in checking presence or absence of mutation in human-derived cytochrome P450IIC18 gene in human-derived cytochrome P450IIC18 gene Fatent: US 5821062-A 1 13-OCT-1998;
Location/Qualifiers
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1 (bases 1 to 18)
Komai,K., Kaneko,H. and Nakatsuka,I.
OLIGONUCLEOTIDE FOR AMPLIFYING MUTATION TYPE GENE OF HUMAN DERIVED
                                                                                                                               CANINE Deta 2- AND beta 3-ADRENERGIC RECEPTORS AND USE THEREOF PATENT: WO 9735973-A 8 02-0CT-1997; VETIGEN (FR)
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                                                                                                          Lenzen,G., Pietri-Rouxel,F., Drumare, Marie-Francoise and
Strosberg,A.D.
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                                                                                                                                                                                  Other publication FR 2746813 19971003.
Location/Qualifiers
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/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
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5821062.
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Sequence 1 from patent US
AR048183
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      A65727
A65727.1 GI:4531346
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Method and reagent for inhibiting the expression of disease related
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Akong, M. Anthony., Harpold, M. Miller., Velicelebi, G. and Brust, P.
Automated analysis equipment and assay method for detecting cell
surface protein function using same
Patent: US 6127131-A 4 03-0CT-2000;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                 Stinchcomb, D.T., Dudycz, L.W., Chowrira, B., Grimm, S., Direnzo, A., Karpeisky, A., Draper, K.G., Kisich, K., Matulic-Adamic, J., Mcswiggen, J.A., Modak, A., Pavco, P., Beigelman, L., Sullivan, S.M., Seedler, D., Thompson, J.D., Tracz, D., Usman, N., Wincott, F.E. and
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 Pred. No. 1.9e+05;
0; Mismatches 1
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Patent: EP 1260586-A 3368 27-NOV-2002;
RIBOZYME PHARMACEUTICALS, INC. (US)
Location/Qualifiers
                                                                                                                                                                                    RNA
                                                                                                                                                                          15 bp RI Sequence 3368 from Patent EP1260586. AX636229 GI:28471843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="unidentified"
/mol_type="unassigned RNA"
/db xref="taxon:32644"
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Sequence 4 from patent US 6127133.
AR111392.1 GI:12828240
92.3%;
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AR111392/c
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AX636229
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Novel g(a) expressed in heart and testis
Patent: WO 204636-A 51 17-JAN-2002;
Vlaams Interuniversitair Instituut voor Biotechnologie vzw. (BE)
Location/Qualifiers
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Stinchoomb, D.T., Draper, K.G. and McSwiggen, J.
Stal a targeted ribozymes
Patent: US 5659780-A 289 19-AUG-1997;
   1
Whittaker,P.A., Jones,S.J. and Hanley,M.T.
Disease-associated gene
Patent: WO 0155214-A 31 02-AUG-2001;
Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
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synthetic construct
other sequences; artificial sequences.
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Sequence 289 from patent US 5658780.
161735
161735.1 GI:2479683
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Sequence 51 from Patent WO0204636.
AX353519
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Best Local Similarity
Matches 14; Conserv
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KEYWORDS

RESULT 14 AX353519 LOCUS

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REFERENCE

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Gaps

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DEFINITION ACCESSION VERSION

RESULT 15 I61735

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KEYWORDS

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ORIGIN

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Gaps

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PAT 15-MAY-2001
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                             Robbins,J.M. and Tritz,R.
Ribozyme therapy for the treatment of proliferative skin and eye
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                                                                                                                                                            1. .19
/organism="Homo sapiens"
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Pred. No. 1.9e+05;
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                                                                                                          Patent: WO 0130362-A 1238 03-MAY-2001;
IMMUSOL, INC. (US)
Location/Qualifiers
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Sequence 1239 from Patent W00130362.
AX130021
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Sequence 43 from Patent WO0164876.
AX269412
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Location/Qualifiers
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Homo sapiens
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nes 12, Conservative
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AX130021/c
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or resistance to viruses and the use thereof as medicaments
Patent: WO 03025177-A 288 27-MAR-2003,
Molecular Engines Laboratories (FR)
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Harpold, M.M. and Brust, P.
Assay methods and compositions useful for measuring the transduction of an intracellular signal
Patent: US 5401629-A 5 28-WAR-1995;
Location/Qualifiers
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Pred. No. 1.9e+05;
0; Mismatches 1;
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Pred, No. 1.9e+05;
0; Mismatches 1;
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Seguence 288 from Patent WO03025177.
AX734698
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WO0130362.
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                                            17 bp
Sequence 5 from patent US 5401629.
AR364674
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AX130020
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Matches 12; Conservative
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Homo sapiens (human)
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Best Local Similarity 92.3
Matches 12; Conservative
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TAGAGTTCTCAGA 3
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AX130020/C
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AX734698/C
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I (bases 1 to 20)
Prockop,D.J., Milliams,C.J., Ritvaniemi,P.,
Prockop,D.J., Ala-Kokko,L., Williams,C.J., Ritvaniemi,P.,
Baldwin,C., Hopkinson,I. and Ahmad,N.Nina.
Primers and methods for detecting mutations in the procollagen II
Primers and methods for detecting mutations for a
COL2A1 that indicate a genetic predisposition for a
COL2A1-associated disease
Patent: US 5948611-A 113 07-SEP-1999;
Location/Qualifiers
                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                               Cohen, D., Blumenfeld, M., Chumakov, I., Abderrahim, H. and Bihain, B. Obesity associated biallelic marker maps
Patent: WO 0206525-A 452 24-JAN-2002;
GENSET (FR)
                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
1. 19
/note="downstream amplification primer 99-48212 for SEQ
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 81.2%; Pred. No. 2.5e+05;
iive 0; Mismatches 3;
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56.0%; Score 11.2; DB 6;

Best Local Similarity 81.2%; Pred. No. 2.5e+05;

Matches 13; Conservative 0; Mismatches 3;
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Sequence 113 from patent US 5948611.
AR072310.
AR072310.1 GI:9999074
                                                                                                                                                                19 bp | Sequence 452 from Patent WO0206525.
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/mol_type="unassigned DNA"
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Homo sapiens
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Best Local Similarity
Matches 13; Conserv
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AR072310
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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1 (bases 1 to 18)

1 (bases 1 to 18)

1 (bases 1 to 18)

Biallelic markers for use in constructing a high density disequilibrium map of the human genome Patent: US 6537751-A 4697 25-MAR-2003;

Location/Qualifiers
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Pred. No. 1.9e+05;
0; Mismatches 1; Indels
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Pred. No. 1.9e+05;
0; Mismatches 1; Indels
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US 6537751.
                    07-SEP-2001;
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
                                                                               /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Sequence 43 from Patent WO0164877.
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/wol_type="genomic DNA"
Human schizophrenia gene
Patent: WO 0164876-A 43 07-SE
Decode Genetics EHF. (IS)
Location/Qualifiers
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Sequence 4697 from patent
AR292962
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92.3%;
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Best Local Similarity 92.3%;
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PAT 12-JUN-2003

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Antitumor antisense sequences directed against R1 and R2 components of ribonucleotide reductase Patent: US 6593305-A 204 15-JUL-2003; Location/Qualifiers
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Unclassified.

I (bases 1 to 20)

Griffais,R., Hoiseth,S.K., Zagursky,R.J., Metcalf,B.J., Peek,J.A.,
Gramaran,B. and Fletcher,L.D.
Chamydia pneumoniae polynucleotides and uses thereof
Patent: US 6552294-A 3744 06-MAY-2003;
Location/Qualifiers
                             1 (bases 1 to 20)
Prockop, D. J., Ala-Kokko, L. and Ritvaniemi, P.
Princkop, D. J., Ala-Kokko, L. and Ritvaniemi, P.
Primers and methods for detecting mutations in the procollagen II
gene that indicate a genetic predisposition for osteoarthritis
Patent: US 5558988-A 113 24-SEP-1996;
Location/Qualifiers
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81.2%; Pred. No. 2.5e+05;
live 0; Mismatches 3;
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Sequence 204 from patent US 6593305.
AR359611.
AR359611.1 GI:33766334
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/organism="unknown"
/mol_type="unassigned DNA"
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/organism="unknown"
/mol_type="genomic DNA"
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AR359611/c
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                                                                                 Unknown.
Unknown.
Unclassified.
I (bases I to 20)
Monia, B.P., Gaarde, W., Ward, D.T. and Cowsert, L.M.
Antisense modulation of MEKK1 expression
Patent: US 6168950-A 36 02-JAN-2001;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                            ch 56.0%; Score 11.2; DB 6; 1. Similarity 81.2%; Pred. No. 2.5e+05; 13; Conservative 0; Mismatches 3;
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Sequence 113 from patent US 5558988.
126421
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                                                             20 bp
Seguence 36 from patent US 6168950.
AR123092
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                                RESULT 27
AR123092/c
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CQ770343
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PAT 17-AUG-2003

4 CGCATAGACTTCTCAG 19

20 CGCAGAGTCTTGTCAG 5

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Unknown. Unclassified.

ORGANISM

KEYWORDS SOURCE

REFERENCE AUTHORS

TITLE

Unknown.

ARSS9459/c LOCUS DEFINITION

RESULT 32

ACCESSION VERSION

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Regulation of repressor genes using nucleic acid molecules.
BD254799
BD254799 IGI:33064569
unidentified
unidentified
          PAT 26-OCT-2001
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                                                                                                                                                                                                                                                                                                                       Hugot, J.P., Thomas, G., Zouali, M., Lesage, S. and Chamaillard, M. Genes involved in intestinal inflammatory diseases and use thereof Patent: WO 0172822-A 82 04-OCT-2001; Fondation Jean Dausset-Ceph (FR)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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PN JP 2002241795-A/2592
PN JP 20022002
PP 11-APR-2000 JP 2000611654
PR 12-APR-1999 US 60/129390
PI LAWRENCE BLATT, MICHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN
C12N15/09, AG1K38/00, AG1K48/00, AG1P43/00, AG1K38/10, PC
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Blatt, L., Zwick, M., Pavco, P. and Mcswiggen, J.
Batt, L., Zwick, M., Pavco, P. and Mcswiggen, J.
Begulation of represent genes using nucleic acid molecules Patent: JP 2002541795-A 2592 10-DEC-2002;
RIBOZYME PHARMACEUTICALS INC
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          linear
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             DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
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20 bp
Sequence 82 from Patent WO0172822.
AX259855
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BD254799
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Antisense Modulation of insulin-like growth factor binding protein 5 expression
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Fondation Jean Dausset-Ceph (FR)
Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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             Length 20;
          Query Match 56.0%; Score 11.2; DB 6; Length 2
Best Local Similarity 81.2%; Pred. No. 2.5e+05;
Matches 13; Conservative 0; Mismatches 3; Indels
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Location/Qualifiers
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Sequence 81 from Patent WO0172822.
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AX259854.1 GI:16508928

AX259854

RESULT 33
AX259854/c
LOCUS
DEFINITION
ACCESSION
VERSION

Homo sapiens (human)

KEYWORDS SOURCE ORGANISM

AUTHORS JOURNAL

REFERENCE

sapiens

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13; Conservative

Best Local Similarity Matches 13; Conserv

Query Match

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Bergeron, M.G., Boissinot, M., Huletsky, A., m Nard, C., Ouellette, M., Picard, F.J. and Roy, P.H.
Highly conserved genes and their use to generate probes and primers for detection of microorganisms
Patent: WO 0123604-A 137 05-APR-2001;
Infectio Diagnostic (I.D.I.) INC. (CA)
                                                                                                                                           (C12P21/02, C12R1:91), (C12P21/02, C12R1:91), C12N15/00, C12N5/00,
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PF 11-APR-2000 JP 2000611654
PR 12-APR-1999 US 60/129390
PI LAWRENCE BLATT, MICHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN PC C12N1S/09, A61K38/00, A61K48/00, A61P43/00, A61P43/00, C12N5/10, PC C12P21/02,
PC C12P21/02, C12P21/02//A61K31/711, (C12N5/10, C12R1:91), (C12P21/02, PC
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(C12N5/00,C12R1:91)
Regulation of repressor genes using nucleic acid molecules FH
Location/Qualifiers
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/nofe="01igonucleotide"
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Sequence 1337 from Patent WO0123604.
AXII0604.1 GI:13926896
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Sequence 32 from patent US 6780609.
AR567503
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/organism="unidentified"
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(C12P21/02,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00,
(C12N5/00,C12R1:91)
Regulation of repressor genes using nucleic acid molecules FH
Location/Qualifiers
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CI2P21/02,C12P21/02//A61K31/711, (C12N5/10,C12R1:91), (C12P21/02, PC
                                                                                                                                                                                                                                                                                                                                                                                                                    PP 11-APR-2000 JP 2000611654
PR 12-APR-1999 US 60/129390
PI LAWRENCE BLATT, MCHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN PC C12N15/09, A61K38/00, A61K48/00, A61P43/00, A61P43/00, C12N5/10, PC C12P21/02,
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unidentified
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unclassified.

E 1 (bases 1 to 17)

S Blatt, L., Zwick, M., Pavco, P. and Mcswiggen, J.

Regulation of repressor genes using nucleic acid molecules
Regulation of repressor 1002541795-A 2593 10-DEC-2002;

PD 10-DEC-2002
PP 11-ARR-2000 PP 20006511654
PR 11-ARR-2000 PP 2000611654
PR 12-APR-1999 US 60/129390
PI LAWRENCE BLATT, MICHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN
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1 (bases 1 to 17)
Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
Regulation of repressor genes using nucleic acid molecules
Patent: JP 2002541795-A 2594 10-DEC-2002;
OS BUARTYOTE
PN JP 2002541795-A/2594
PD 10-DEC-2007
                                                                                                                                 BDIS4800 17 bp DNA linear PAT 17-Regulation of repressor genes using nucleic acid molecules.
BD254800
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100.0%; Pred. No. 3.3e+05;
iive 0; Mismatches 0;

    .17
    /organism="unidentified"
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   iM Unknow...
Unknow...
Unclassified.
E 1 (bases 1 to 18)
S Carulli,J.P., Little,R.D., Recker,R.R. and Johnson,M.L.
High bone mass gene of 1.1q13.3
IL Patent: US 6780609-A 32 24-AUG-2004;
S Location/Qualifiers
urce /organism="unknown"
/mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 55.0%; Score 11; DB 6; Length 18; 100.0%; Pred. No. 3.3e+05; Live 0; Mismatches 0; Indels
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/organism="synthetic construct"
/organism="synthetic DNA"
/ol_type="unassigned DNA"
/db_xref="taxon:22630"
/note="Artificial sequence is a primer."
                                                                                                                                                                                                                                                                                                                                                                           DNA
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synthetic construct
other sequences; artificial sequences.
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Matches 11; Conserva
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Aav30475 Canine be Aav3305 Primer CT Aaz24116 Primer CT Abz21284 Human oli Abd27514 AA486238-Ad417514 AA486238-Ad417514 AA486238-Ad417514 Human CTN Ab559713 Human CTN Ad57865 Chimeric Ad47865 Chimeric Ad47865 Chimeric Ad47865 Chimeric Ad47865 Chimeric Ad47865 Chimeric Ad47865 Chimeric Ad47785 Human tum Aa83652 cdk-we-hu Aab58815 cdk-we-hu Aab58815 cdk-we-hu Aab58815 cdk-we-hu Ad661886 Anti-KCNH AA59121 Human DNA AA60823 Human neu Ad6129181 Human neu Ad6129181 Human neu Ad612918 Human CYP Ad612915 Human CYP Ad612915 Human CYP Ad612515 Human CYP Ad612515 Human CYP Ad612515 Human TNF Ad61251 PCR Prime Ad133817 Human TNF Ad61251 PCR Prime Ad18651 PCR Prime Ad46651 PCR Prime Ad18651 AAZ 70341 Human Dia Ab441204 Human obe Aag65840 Type II p Aa202195 PCR prime Aa290858 Ribonucle Aa427114 Human MEK Aa16569 Primer fo Aa16569 Primer fo Aa16569 Primer fo Aa16569 Human II-Ab286038 Human oli Ab286038 Human oli Ab28269 Human IGF Ab62268 Human IGF Ad62268 Human IGF AAA83652 AAH58814 AAH58815 ADQ61886 ADH77528 ADK95401 ADP43749 ACC74121 ACC74122 ADB89105 ADC24452 ADD67722 ADE10435 ADE11357 ADE12535 ADE12298 ADG25432 ADJ47831 ADJ 61852 ADF 5288 ADF 3293 ADG 43293 ADG 43550 ADG 6614 ADI 12846 ADI 12846 ADI 27748 ADI 27748 ADI 3817 ADI 3817 ADI 3817 ADI 3817 ADI 3817 ADM46269 AAZ70341 ABK41204 AAD11750 ABK41518 ABS59713 ADK78853 ADK78852 ADK78852 AAT55168 ACA09062 ABT01507 ADI29181 ADI29115 AAQ65840 AAZ02195 AAX94418 AAA90858 AAF27114 AAI65670 AAI65669 AAD08233 AAK96737

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The present sequence is the human PB39 3' specific RACE primer, from EST clone AAR00504. It is used to determine the complete nucleotide sequence of PB39 coNRA, isolated from human pancreas cDNA library using RACE. The PB39 gene that is dysregulated in prostate cancer has homology to the EST AAR00504. PB39 gene is located on chromosome lipli.1-11.2. Abnormally high concentrations of PB39 are found in prostate tissue derived from prostate cancer (PC) epithelium. PB39 sequence is useful for detection of presencerous or cancer cells in the prostate. PB39 is useful for early diagnosis of the progression of prostate cancer, especially in aggressive prostate carcinoma. It can also distinguish PC from other non-neoplastic prostate disease. The diagnostic method is selective and specific for various types of PC and also facilitates identifying prostate cancer of
             Aaf02601 Hammerhea
Aaf02603 Hammerhea
Aaf02602 Hammerhea
Aah01346 parc resi
Aba82646 Human Zma
Aba82604 HBM1 poly
                                                                                                                                                                                                                                                                                                                           PB39; human; prostate cancer; PC; chromosome 11p11.1-11.2; cancer; prostate epithelium; splicing mechanism; early diagnosis; progression; precancerous cell; metastatic potential; non-neoplastic prostate disease; expressed sequence tag; EST; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel gene which is dysregulated in prostate cancer useful for diagnosing
Ad127440
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                                                                                                                                  ALIGNMENTS
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 ADL27440
               AAF02601
AAF02603
AAF02602
AAH01346
ABA82646
                                                                                                                                                                                                                                                                                               Human PB39 specific 3' RACE primer.
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 (first entry)
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Best Local Similarity 100.
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AAX91991-X97517 represent PCR primers used to amplify open reading frames and other nucleic acid sequences from the genome of Chlamydia pneumoniae (see AAX91990). C. pneumoniae causes respiratory disease such as pneumonia and bronchitis and is thought to be a contributing factor in heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema nodosum or pharyngitis. The polypeptides encoded by the open reading frames of the C. pneumoniae genome (see AN34584 - AAX35879) can be used in immunogenic compositions as vaccines. Vectors containing C. pneumoniae especially where the vector directs the expression of a neutralising
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                                                                                                                                 Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis; sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine; neutralising epitope; PCR primer; ss.
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                                                                                                      PCR primer used to amplify an ORF of Chlamydia pneumoniae.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genome sequence of Chlamydia pneumoniae.
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88.2%;
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               AAX93486 standard; DNA; 20
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Matches 15, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                    (GEST ) GENSET
                                                                                                                                                                                                                                                                                                         20-NOV-1998;
                                                                                                                                                                                                                                                                                                                                       21-NOV-1997;
                                                                                                                                                                                                                                               WO9927105-A2
                                                                                                                                                                                                                                                                                                                                                      04-NOV-1998;
                                                                          13-SEP-1999
                                                                                                                                                                                                                                                                           03-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                  Griffais R;
                                                                                                                                                                                                  Synthetic
                                            AAX93486;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAD62200;
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AAX93486
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Gaps

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0; Indels

0; Mismatches

GACCGCATAGACTTCTCAGA 20 GACCGCATAGACTTCTCAGA 20

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This invention relates to a novel activated mutant protein tyrosine kinases and associated methods for diagnosing cancer and screening for tumourigenesis. Mutational analysis of the human tyrosine kinase gene family identified somatic alteration sin 1 in 5 colorectal cancers, with the majority of mutations occurring in the NTRK1. FES, GUCY2F and MCCK/MLK4 genes. Most were identified in the kinase domain. The invention may be useful for the production of compounds with a cytostatic activity acting as protein tyrosine kinase inhibitors or guanylate cyclase acting as protein tyrosine kinase inhibitors or guanylate cyclase detecting mutations involved in cancer or screening for anti-cancer agents. The present sequence is that of a human-derived oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Enzymatic nucleic acid; nuclear factor kappa B; NFKB; inozyme; zinzyme; G-cleaver; amberzyme; cancer; REL-A activity; breast cancer; lung cancer; prostate cancer; colorectal cancer; brain cancer; oesophageal cancer; stomach cancer; bladder cancer; pancreatic cancer; cervical cancer; head and neck cancer; ovarian cancer; melanoma; lymphoma; glioma;
                                                                                                     tyrosine kinase, cancer; anti-cancer agent, signalling molecule;
tumourigenesis; somatic alteration; colorectal cancer; NTRK3; FBS;
GUCY2F; MCCK; MLK4; kinase domain; cytostatic; tyrosine kinase inhibitor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Activated mutant protein tyrosine kinases (e.g. NTRK3, FES and MCCK) and associated methods for diagnosing cancer and screening for anti-cancer
                                                          Novel mutant protein tyrosine kinase-related oligonucleotide SeqID428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Necrosis factor kappa B (NFKB) sub-unit modulating DNAzyme #56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63.0%; Score 12.6; DB 13; Length 20; 78.9%; Pred. No. 1e+04; ive 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seguence 20 BP; 4 A; 7 C; 5 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; SEQ ID NO 428; 363pp; English,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Velculescu V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            which is related to the invention.
                                                                                                                                                                            guanylate cyclase stimulator; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GACCGCATAGACTTCTCAG 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACA08287 standard; DNA; 17 BP
                                                                                                                                                                                                                                                                                                                                                               18-FEB-2004; 2004WO-US004452
                                                                                                                                                                                                                                                                                                                                                                                                         21-FEB-2003; 2003US-0448537P
                                                                                                                                                                                                                                                                                                                                                                                                                               29-MAY-2003; 2003US-0473895P
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                  (first entry)
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Best Local Similarity 78.9
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2004-718702/70.
                                                                                                                                                                                                                                                                     WO2004082458-A2
                     16-DEC-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bardelli A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACA08287;
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ACA08287
ID ACA08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a compound targetted to a nucleic acid molecule encoding haematopoietic cell protein tyrosine kinase. The compound inhibits the expression of haematopoietic cell protein tyrosine kinase and it specifically hybridises with the nucleic acid molecule encoding the tyrosine kinase or with at least an 8-nucleobase portion of an active site on the nucleic acid molecule encoding the tyrosine kinase. The antisense compounds are useful for modulating the expression of ammatopoietic cell protein tyrosine kinase and treating diseases or conditions associated with the expression of the tyrosine kinase, such as typerprofiferative disorders (e.g. cancer), inflammation, diabetes or a viral infection. The antisense compounds are also useful for diapnostics, therapeutics, prophylaxis, e.g. to prevent or delay infection, distinguishing between functions of various members of a biological pathway. The present sequence is human haematopoietic cell tyrosine kinase antisense oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                     /nore= "Phosphorothioate backbone; All cytidines are 5-methyl cytidines"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New antisense oligonucleotides targeted to nucleic acids encoding thematopoietic cell protein tyrosine kinase, useful for diagnosing treating cancer (e.g. leukemia), inflammation, diabetes or viral infections.
                                                                                                                                                                                                                                                         /mod_base= OTHER
/note= "2'-O-methoxyethyl (2'-MOE) nucleotides"
16. .20
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                                                                                                                                                                                                                                                                                                                                                                                  /note== "2'-0-methoxyethyl (2'-MOE) nucleotides'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 20 BP; 6 A; 2 C; 7 G; 5 T; 0 U; 0 Other;
                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 15; Page 26; 59pp; English
                                                                                                                                                                                                                                                                                                                                                                 base= OTHER
                                                                                                                                                      /mod_base= OTHER
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/*tag=
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                                                                                                                                                                                                                                                                                                                                                                    /mod
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tes 15; Conserv
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                                                                                         Key
modified_base
                                                                                                                                                                                                                             modified base
                                                                                                                                                                                                                                                                                                                    modified base
                     Homo sapiens.
Synthetic.
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Vogelstein B;

Kinzler KW,

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Gaps

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Query Match

Matches

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ADT00440

ADT00440 RESULT

ACA06680

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The invention describes an enzymatic nucleic acid molecule (1) which down regulates expression of a sequence encoding a subunit of nuclear factor kappa B (NFRA), where (1) is an inozyme, zinzyme, G-cleaver or amberzyme configuration. The enzymatic nucleic acid molecule is adapted to treat cancer and is useful for down-regulating REL-A activity in a cell, for treating a patient having a condition associated with the level of REL-A. (1) is useful for cleaving RNA comprising a sequence of REL-A gene, in the presence of a divalent cation, especially MG^2+. The enzymatic and antisense nucleic acid molecules are useful for treating breast, lung, prostate, colorectal, brain, oesopageal, stomach, bladder, pancreatic, crivial, head and neck, ovarian cancer, melanoma, lymphoma, glioma or multidrug resistant cancer. The method involves use of other drug theraphes such as monoclonal antibodies, REL-A-specific inhibitors or chemotherapy including paclitaxel, docetaxel, cisplatin, methotrexate, gencitabline or radiation therapy. The enzymatic and antisense nucleic acid also useful for treating inflammatory disease such as each as a contract of the contract of an antisense nucleic acid antistic and antisense molecic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel enzymatic nucleic acid molecules which down regulates expression of
multidrug resistant cancer; REL-A-specific inhibitor; chemotherapy; paciltaxel; docetaxel; cisplatin; methotrexate; cyclophosphamide; doxorubin; fluorouracil carboplatin; edatrexate; gemcitabine; radiation therapy; inflammatory disease; asthma; diabetes; rheumatoid arthritis; restenosis; Crohn's disease; obesity; ischaemia; gene therapy; autoimmune disease; lupus; multiple sclerosis; sepsis; transplant/graft rejection; reperfusion injury; glomerulonephritis; allergic airway inflammation; inflammatory bowel disease; infection; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rheumatoid arthritis, restenosis, asthma, Črohn's disease, diabetes, obesity, autoimmune disease, lupus, multiple sclerosis, transplant/graft rejection, gene therapy applications, ischaemia/reperfusion injury (central nervous system (CNS) and myocardial), glomerulonephritis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              intection. This sequence represents an enzymatic nucleic acid used t modulate the function of a necrosis factor kappa B sub-unit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           a sequence encoding a subunit of nuclear factor kappa B useful for treating cancer, inflammatory disorders and autoimmune diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (central nervous system (CNS) and myocardial), glomerulonephritis, sepsis, allergic airway inflammation, inflammatory bowel disease o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Draper KG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 3; Page 46; 72pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                        94US-00245466.
94US-00291932.
96US-00777916.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mcswiggen J,
                                                                                                                                                                                                                                                                                                                                                       23-MAY-2001; 2001US-00864785
                                                                                                                                                                                                                                                                                                                                                                                                     92US-00987132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STINCHCOMB D T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MCSWIGGEN J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-340953/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DRAPER K G.
                                                                                                                                                                                                                                                               US2002177568-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Stinchcomb DT,
                                                                                                                                                                                                                                                                                                                                                                                                                             .8-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                     07-DEC-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-DEC-1996;
                                                                                                                                                                                                                                                                                                            28-NOV-2002
                                                                                                                                                                                                                    Synthetic.
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(DRAP/)
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                                                             Gaps
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0
                             62.0%; Score 12.4; DB 8; Length 17; 64.3%; Pred. No. 1.3e+04; cive 4; Mismatches 1; Indels
Sequence 17 BP; 4 A; 4 C; 5 G; 0 T; 4 U; 0 Other;
                                                                                              CATAGACTTCTCAG 19
                                                                                                                CAUGGACUUCUCAG 17
                                                Local Similarity 64.3
nes 9; Conservative
                                                                                                9
                                  Query Match
                                                 Best Loc
Matches
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RESULT 6

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The invention describes an enzymatic nucleic acid molecule (I) which down regulates expression of a sequence encoding a subunit of nuclear factor regulates expression of a sequence encoding a subunit of nuclear factor regulation. The enzymatic nucleic acid molecule is adapted to treat configuration. The enzymatic nucleic acid molecule is adapted to treat cancer and is useful for down-regulating REL-A activity in a cell, for treating a patient having a condition associated with the level of REL-A.

(I) is useful for cleaving RNA comprising a sequence of REL-A gene, in the presence of a divalent cation, especially Mg^2+. The enzymatic and antisens nucleic acid molecules are useful for treating breast, lung, corrical, head and neck, ovarian cancer, melanoma, lymphoma, glioma or cantisense nucleic acid molecules are introduced. REL-A-specific inhibitors or therapies such as monoclonal antibodies, REL-A-specific inhibitors or chemotherapy including paclicaxel, docetaxel, cisplatin, methocrexate, cyclophosphamde, docorubin, fluorouracil carboplatin, edatrexate, cyclophosphamde, docorubin, methodrexate, cyclophosphamde, docorubin, genethoracy are also useful for treating inflammatory disease such as colection, gene therapy applications, ischaemia/reperfusion injury (central nervous system (CNS) and myocalminal), glomerulonephritis, cobesity, allergic airway inflammation, inflammatory bowel disease or infection. This sequence represents the substrate of a novel enzymatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel enzymatic nucleic acid molecules which down regulates expression of a sequence encoding a subunit of nuclear factor kappa B useful for treating cancer, inflammatory disorders and autoimmune diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                     gencitabine, radiation therapy, inflammatory disease, asthma; diabetes, rheumatoid arthritis, restemosis, Crohn's disease, obesity, ischaemia, gene therapy, autoimmune disease, lupus, multiple sclerosis, sepsis, transplant/graft rejection, reperfusion injury, glomerulonephritis, allergic airway inflammation, inflammatory bowel disease, infection; se
                                                                                                                                                                                                                                   G-cleaver; amberzyme; cancer; REL-A activity; breast cancer; human; lung cancer; prostate cancer; colorectal cancer; brain cancer; cosphageal cancer; stomach cancer; bladder cancer; pancreatic cervical cancer; stomach cancer; ovarian cancer; melanoma; cervical cancer; head and neck cancer; ovarian cancer; melanoma; lymphoma; gliona; multidrug resistant cancer; REL-A-specific inhibitor; chemotherapy; paclitaxel; docetaxel; cipplatin; methotrexate; cyclophosphamide; doxorubin; fluorouracil carboplatin; edatrexate;
                                                                                                                                                                                                          Enzymatic nucleic acid; nuclear factor kappa B; NFKB; inozyme; zinzyme;
                                                                                                                                                         NFKB sub-unit modulating inozyme substrate #499.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 3; Page 34; 72pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            92US-00987132.
94US-00245466.
94US-00291932.
96US-00777916.
ACA06680 standard; RNA; 17 BP.
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                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (MCSW/) MCSWIGGEN J. (DRAP/) DRAPER K G.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5-AUG-1994;
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                                                    ACA06680;
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Query Match

Matches

ઠ 셤 AAZ48549;

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The invention relates to an antisense compound 8 to 30 nucleotides in length targeted to nucleic acid molecule encoding tumour necrosis factor receptor 1 (TMFR1), where the antisense compound inhibiting the expression of TMFR1. The antisense compound is useful for inhibiting the expression of TMFR1 in cells or tissues. The antisense compound is also useful for treating an animal (preferably human) having a disease or condition associated with TMFR1, e.g. a liver disease (such as hepatitis, or liver injury) or a hyperproliferative disorder such as cancer, by inhibiting disagnostics, therapeutics, prophylaxis and as research reagents and kits. This polymucleotide sequence represents a human oligonucleotide relating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel antisense compound targeted to nucleic acid molecule encoding tumor necrosis factor receptor 1 (TNFR1), useful for treating humans having disease associated with TNFR1 e.g. hepatitis, liver injury, liver cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cytostatic; gene therapy, apoptosis inhibitor; radiation-induced apoptosis; tumour necrosis factor receptor 1; TNFR1; human; antisense oligonucleotide; antisense technology; ss.
                                                                                                                          Antisense compound; tumour necrosis factor receptor 1; liver disease; TNFR1; hepatitis; liver injury; hyperproliferative disorder; cancer; human; ds.
                                                                                                  INFR1 expression modulation related antisense oligo SEQ ID No 75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 12.2; DB 6; Length 18;
Pred. No. 1.6e+04;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 18 BP; 5 A; 3 C; 7 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human TNFR1 antisense oligonucleotide seqid 75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dean NM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 10; Page 45; 121pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zhang H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to the TNFR1 of the invention
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82.4%;
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                                                           11-OCT-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cowsert LM,
                                                                                                                                                                                                                                                                                                                                                                                                                                          (ISIS-) ISIS PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-583481/62.
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Best Local Similarity
                                                                                                                                                                                                                                                                      WO200248168-A1
                                                                                                                                                                                                                                 Ното варіепв.
                                                                                                                                                                                                                                                                                                               20-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Baker BF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADR06077;
                   ABT05045;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADR06077/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention provides antisense compounds targeted to human tumour necrosis factor receptor type 1 (TNFR1) RNA. These antisense compounds can be used in a method of inhibiting the expression of TNFR1 human cells or tissues. The antisense compounds specifically hybridize with one or more nucleic acids encoding TNFR1 modulating the function of nucleic acid molecules encoding TNFR1, ultimately modulating the amount of TNFR1 produced. The antisense compounds and method are useful as research reagents and diagnostics, and in the treatment and prophylaxis of infection, inflammation or tumour formation. Sequences AAZ48482-565 represent antisense oligos used for inhibition of the human TNFR1 mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tumour necrosis factor receptor type 1; TNFR1; antisense; infection; inflammation; tumour formation; TNFR1; anticancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antisense inhibition of tumor necrosis factor type 1 expression for diagnosis, treatment and prevention of disease, particularly tumors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                              62.0%; Score 12.4; DB 8; Length 17; 64.3%; Pred. No. 1.38+04; ive 4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61.0%; Score 12.2; DB 3; Length 18; 82.4%; Pred. No. 1.6e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                            Human TNFR1 mRNA inhibiting antisense oligo ISIS# 18942.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 18 BP; 5 A; 3 C; 7 G; 3 T; 0 U; 0 Other;
                                       Sequence 17 BP; 4 A; 6 C; 3 G; 0 T; 4 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 10; Col 25; 34pp; English.
                                                                                                                                                                                                                                                                                                                    ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 CGCATAGACTICTCAGA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98US-00106038
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                                                                                                                                                                                                                                                                                                                 AAZ48549 standard; DNA; 18
                                                                                                                                                                 6 CATAGACTICICAG 19
                                                                                                                                                                                         ||: |||::|:|||
CAUGGACUUCUCAG 15
                                                                                                                                                                                                                                                                                                                                                                                                  31-MAR-2000 (first entry)
                                                                                                    Local Similarity 64.3
Les 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cowsert LM;
nucleic acid molecule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-105333/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-JUN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Baker BF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic
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Gaps

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Homo sapiens

5045/c ABT05045 standard; DNA; 18

ABT05045/ ID ABT0

Query Match Matches

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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Inhibiting radiation-induced apoptosis in a cell or tissue comprises administering to the cell or tissue an antisense oligonucleotide targeted to a nucleic acid molecule encoding tumor necrosis factor receptor 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   apoptosis in a cell or tissue comprising administering to the cell or tissue an antisense oligonucleotide of 8-30 nucleotides in length targeted to a nucleic acid molecule encoding tumour necrosis factor receptor 1 (TNFR1). The method and antisense oligonucleotides are useful for inhibiting radiation-induced apoptosis in a cell or tissue, and for treating diseases associated with the expression of TNFR1. This sequence represents a human tumour necrosis factor receptor 1 (TNFR1) antisense
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                  /mod_base= OTHER
/note= "OTHER= Optionally 2'-0-Methoxyethyl (2'-MOE)
nuclectides"
                                                                                                                                                                                                                                             /mod_base= OTHER
/note= "OTHER= Optionally 2'-O-Methoxyethyl (2'-MOE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Avr; Hop; transgenic plant; disease resistance; cancer; bacteria; metabolic pathway; eukaryotic cell death; programmed cell death; cytostatic; PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention describes a method of inhibiting radiation-induced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pseudomonas syringae pv. tomato DC3000 Hop gene PCR primer #40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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                                                                              'note= "OTHER= Phosphorothioate backbone"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 18 BP; 5 A; 3 C; 7 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 10; SEQ ID NO 75; 24pp; English
Location/Qualifiers
                                                           /mod_base= OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20
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17-JUN-1999; 99WO-US013763
24-OCT-2000; 2000US-00695451.
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                                                                                                                                                                                                                                                                                      nucleotides'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGCATAGACTTCTCAGA
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                                                                                                                                                                                                         15. .18
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   oligonucleotide
                                                                                                                                                                                                                                                                                                                              US2004147471-A1
  Key
modified_base
                                                                                                   modified base
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  SOCCOCCCC X S X X B X X B X X B X X B X X B X X B X X B X B X B X X B X X B X X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B 
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New nucleic acid, useful in imparting disease resistance to a plant or in preparing a composition for treating cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Pred. No. 1.6e+04;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Cartinhour SW, Schneider DJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cytostatic; gene therapy; Avr; Hop; cancer; primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seguence 19 BP; 4 A; 7 C; 4 G; 4 T; 0 U; 0 Other;
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Pseudomonas syringae; pv. tomato str. DC3000
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10-MAY-2002; 2002US-0380185P.
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                                                                                                                                                           12-FEB-2003; 2003US-00365742.
                                                                                                                                                                                                         2002US-0356408P.
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82.4%;
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                                                                                                                                                                                                                                                                                                             ALFANO J R. CARTINHOUR S W. SCHNEIDER D J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Collmer A, Alfano JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-875735/81
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Best Local Similarity
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                                                        US2003204868-A1
                                                                                                                                                                                                                                                                                                                                                                                           TANG X.
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                                                                                                                                                                                                                                                                                                                                                                   (SCHN/)
(TANG/)
                                                                                                                                                                                                                                                                                                               (ALFA/)
(CART/)
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HMG-CoA reductase; 3-hydroxy-3-methylglutaryl-Coenzyme A;
HMG-CoA reductase; cardiant; antiarteriosclerotic; antilipaemic;
antisense gene therapy; cardiovascular disorder; cholesterol metabolism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to novel compounds of 8-80 nucleobases in length targeted to, and which specifically hybridises with, a nucleic acid molecule encoding 3-hydroxy-3-methylglutaryl-Coenzyme A (HMG-CoA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New compounds, particularly antisense oligonucleotides targeted to
nucleic acid encoding HMG-COA reductase, useful for treating
atherosclerosis, or a disease involving cholesterol metabolism or
                                                                                                                                                                                                                                                                                                                                                                                                                                  Mouse HMG-CoA reductase antisense oligonucleotide, SEQ ID No 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 16; SEQ ID NO 389; 110pp; English.
                                                                                                                                                                                                                                                                                                                                                                     ADI79866 standard; DNA; 20 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-JUL-2002; 2002US-00190366.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-JUL-2002; 2002US-00190366.
                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
SEC OF AGRIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ISIS-) ISIS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dean NM, Freier SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2004-081743/08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mouse; murine; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US2004006031-A1.
                                                                                               treating cancer
                                                                                                                                                                                                       the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     angiogenesis
                                                                                                                                                                                                                                                                                                                                                                                                               22-APR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-JAN-2004
as
                                         Collmer A,
                                                                                                                                                                                                                                                                                                                                                                                          ADI 79866;
                                                                                                                                                                                                                                                Query Match
(USDA)
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Matches
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Dobie KW

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reductase, and inhibits the expression of HMG-CoA reductase. The novel compounds have cardiant, antiarteriosclerotic, and antilipaemic cartivities. The compound can be used to treat disorders by antisense gene therapy. The compounds, compositions and methods are useful for treating a disease or condition associated with HMG-CoA reductase, such as a cardiovascular disorder e.g. atherosclerosis, or a disease or condition involving cholesterol metabolism. They are also useful in research and diagnostics for modulating the expression of HMG-CoA reductase. This polymocleotide sequence represents an antisense oligonucleotide of the
                                                                                                                                                                                                                                                                                                                            Sequence 20 BP; 6 A; 6 C; 4 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                               1 Similarity 82.4%;
14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 CGCATAGACTTCTCAGA
                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 14; Conserv
                                                                                                                                                                                                                                                                            invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADI79673;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 13
ADI79673/c
                 888888888888888
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to novel Pseudomonas Avr and Hop genes, a sequence that hybridizes with these sequences under stringency conditions comprising a hybridization medium that includes 0.9 x saline sodium citrate (SSC) buffer at a temperature of 42 deg C. The nucleic acid molecule is useful for preparing a composition for treating cancer. This sequence corresponds to a PCR to isolate and amplify one of the genes of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                 New nucleic acid molecule, useful for preparing a composition for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                Tang X;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          / Match 61.0%; Score 12.2; DB 10; Length 19; Local Similarity 82.4%; Pred. No. 1.6e+04; nes 14; Conservative 0; Mismatches 3; Indels
                                                                                                                                   Schneider DJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 19 BP; 4 A; 7 C; 4 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                     Disclosure; SEQ ID NO 187; 284pp; English.
                                                                                                                                   Cartinhour SW,
                                            (UTNE-) UNIV NEBRASKA.
(UNIV ) UNIV KANSAS STATE RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 CCGCATAGACTICTCAG 19
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                                                                                                                                   Alfano JR,
                                                                                                                                                                                           WPI; 2003-679632/64
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Length 20; Indels

Score 12.2; DB 12; Pred. No. 1.6e+04;

61.0%;

0; Mismatches

20

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The invention relates to novel compounds of 8-80 nucleobases in length targeted to, and which specifically hybridises with, a nucleic acid molecule encoding 3-hydroxy-3-methylglutary1-Coanzyme A (HMG-COA) reductase, and inhibits the expression of HMG-COA reductase. The novel compounds have cardiant, antiatreriosclerotic, and antilipaemic activities. The compounds compositions and methods are useful for treating a disease or condition associated with HMG-COA reductase, such as a cardiovascular disorder e.g. atherosclerosis, or a disease or condition involving cholesterol metabolism. They are also useful in research and diagnostics for modulating the expression of HMG-COA reductase. This involvule esquence represents an antisense oligonucleotide of the invention.
                                                                                                                                                                                                                                 HMG-CoA reductase; 3-hydroxy-3-methylglutaryl-Coenzyme A;
HMG-CoA reductase; cardiant; antiarteriosclerotic; antilipaemic;
antisense gene therapy; cardiovascular disorder; cholesterol metabolism;
mouse; murine; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New compounds, particularly antisense oligonucleotides targeted to nucleic acid encoding HMG-CoA reductase, useful for treating atherosclerosis, or a disease involving cholesterol metabolism or
                                                                                                                                                                                               Mouse HMG-CoA reductase antisense oligonucleotide, SEQ ID No 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 16; SEQ ID NO 196; 110pp; English
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          13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-JUL-2002; 2002US-00190366.
CACAGAGACTCCTCAGA
                                                                                             ADI79673 standard; DNA; 20
                                                                                                                                                                  22-APR-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ISIS-) ISIS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Freier SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2004-081743/08
                                                                                                                                                                                                                                                                                                                                                             US2004006031-A1
                                                                                                                                                                                                                                                                                                                             Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            angiogenesis.
                                                                                                                                                                                                                                                                                                                                                                                               08-JAN-2004
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Matches

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RESULT 14 AAQ32840

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comprising the repeat polymorphisms in an amount effective for testing polymorphisms. The method comprises obtaining polymucleotide segments comprising the repeat polymorphisms in an amount effective for testing and amplifying the segments by a PCR procedure using a pair of sequence. The amplified sequences are resolved using PAGE and the resolved sequences are compared by autoradiography to observe the differences in migration pattern due to length variation. The polymucleotides provide a fast and accurate test for measuring the subtle differences in individuals in eg. forensic screening, paternity and prenatal screening and genetic mapping. The polymucleotides are specific for polymorphic microsatellite repeats based on previously sequenced human genes. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                          Primer; assay; subtle difference; dinucleotide; tetranucleotide; repeat; polymorphism; PCR; polymerase chain reaction; amplify; PAGE; autoradiography; migration pattern; length variation; genetic mapping; forensic screening; paternity; prenatal; screening; microsatellite;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The sequences given in AAQ57782-866 are primers which were used in an assay for measuring the subtle differences in genetic material regarding an added or omitted set of dinucleotide or tetranucleotide repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New polynucleotide sequences - derived from polymorphic micro:satellite repeats, used for characterising human individuals for forensic, paternity and prenatal screening and genetic mapping.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          neoplasia; mutant; target nucleotide; hybridization; lung cancer; 88; neck cancer; head cancer; saliva test; chemotherapy; early detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60.0%; Score 12; DB 2; Length 20; 75.0%; Pred. No. 2.1e+04; rive 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 20 BP; 6 A; 8 C; 3 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Exemplary oligonucleotide primer TBP (For).
                                                       Primer pair 26A II-D detection primer #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         (USSH ) US DEPT HEALTH & HUMAN SERVICES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 47; 72pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GACCGCATAGACTTCTCAGA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GACCCCACAGCCTATTCAGA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Merril CR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BP.
                                                                                                                                                                                                                                                                                                                                                                                           92US-00922723.
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Matches 15; Conservative
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                   (first entry)
(revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1994-065727/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Polymeropolous MH,
                                                                                                                                                                                                                                                                     WO9403640-A1
                                                                                                                                                                                                                                                                                                                                                     30-JUL-1993;
                                                                                                                                                                                                                                                                                                                                                                                             31-JUL-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                   28-SEP-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-DEC-1999
25-MAR-2003
                   21-AUG-1994
                                                                                                                                                                                                                                                                                                              17-FEB-1994
                                                                                                                                                                                      human; ss.
                                                                                                                                                                                                                               Synthetic.
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ID AAZ2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oligo-nucleotide primers for polymerase chain reaction amplification - which detect DNA polymorphisms and are useful for prenatal and paternity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This is a PCR primer which is used (with AAQ32841) to characterise a unique microsatellite repeat polymorphic DNA marker which has a high polymorphism information content. The marker is useful for human individualisation, in forensic screening, in paternity and prenatal screening as well as in genetic mapping. (Updated on 25-MAR-2003 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIC; high polymorphism information content; forensic; screening; polymerase chain reaction; genetic mapping; paternity; prenatal.
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0
                                                              Length 20;
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60.0%; Score 12; DB 2; Length 20;
Best Local Similarity 75.0%; Pred. No. 2.1e+04;
Matches 15; Conservative 0; Mismatches 5; Indels
                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                      Microsatellite repeat polymorphic DNA marker PCR primer.
                                          Score 12.2; DB 12;
Pred. No. 1.6e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 20 BP; 6 A; 8 C; 3 G; 3 T; 0 U; 0 Other;
                     Sequence 20 BP; 4 A; 4 C; 6 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (USSH ) US DEPT HEALTH & HUMAN SERVICE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig 60; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GACCGCATAGACTTCTCAGA 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           screening, and genetic mapping.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Polymeropoulos MH, Merrill CR
                                                                                                                                               20
                                                                                                                                                                                                                                                                                           BP.
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91US-00799828.
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                                                         Match 61.0%;
Local Similarity 82.4%;
es 14; Conservative
                                                                                                                                             4 CGCATAGACTTCTCAGA
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                                                                                                                                                                                                                                                                                                                                                                            (revised)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-MAY-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-NOV-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-MAY-1992;
                                                                                                                                                                                                                                                                                                                                                                          25-MAR-2003
05-MAY-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                                   AAQ32840;
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                                                            Query Match
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RESULT 15

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AAQ57863

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WO2003040369-A2
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04-DEC-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Telerman A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             diagnosis.
         Smith MW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADB42063;
                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 18
                                                                                                                                                                                                                                                                                                                                                                                                                           ADB42063
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                                                                                                                                                                                               Detection of cancers comprises assaying for a genetic mutation associated
                                                                                                                                                                                                                                             This is an exemplary oligonucleotide primer, for use in the detection of neoplasmic related gene mutations. There are over 40 known proto-
oncogenes and suppressor genes to date, which control growth,
development, and cell differentiation. Regulation of these genes can,
under certain circumstances, be altered and normal cells can assume
neoplastic growth characteristics. The invention provides a method for
detecting a neoplastic disorder of the head and neck or lung in a
subject. The detection of a target mutant nucleotide sequence in the
saliva is indicative of a neoplastic disorder of the head, neck or lung.
This allows early detection and therefore treatment of the preneoplasia
or cancer, and can also be used to monitor high risk patients undergoing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Short tandem repeat, primer, STR; susceptibility; HIV; infection; AIDS; detection, polymorphism; interleukin 10 promoter; IL-10, chromosome position 6q27; TATA box-binding protein; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TATA box-binding protein short tandem repeat primer SEQ ID NO:23.
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                                                                                                                                                                                                                                                                                                                                                                                                    Match 60.0%; Score 12; DB 2; Length 20; Local Similarity 75.0%; Pred. No. 2.1e+04; les 15; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                   Sequence 20 BP; 6 A; 8 C; 3 G; 3 T; 0 U; 0 Other;
                                                                                                                                 (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                             Disclosure; Page 27; 99pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GACCGCATAGACTTCTCAGA 20
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                                                                                                                                                                                                                                                                                                                                                                 chemoprevention or chemotherapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAC60963 standard; DNA; 20 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-APR-2000; 2000WO-US009355
                                                                                            99WO-US005220
                                                                                                               98US-00038637
 primer; PCR; amplification
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                Homo sapiens
                                                   WO9946408-A1
                                                                                            LO-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-0CT-2000
                                                                                                                                                      Sidransky D;
                                                                                                                                                                                                           with cancer.
                                                                       16-SEP-1999
                     Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAC60963;
                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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The present invention describes a method for predicting susceptibility to

HIV infection or HIV progression in a subject. The method involves

Getecting a polymorphism in a human interleukin-10 (IL-10) promoter,

where the presence of the polymorphism indicates susceptibility to HIV

infection or HIV progression. The method provides prognostic information

to persons infected with HIV virus and is useful to help select

treatments (sunch as administration of IL-10 or gene therapy with IL-10).

The presence of polymorphism is useful as predictor that very aggressive

treatment could substantially eradicate the virus from the infected

person. The method is useful for the generation of normograms or other

predictive algorithms that can be used, in association with allele

crantus, to prognose probable survival or years to development of AIDS

following HIV seroconversion. It indicates that increased expression of

the IL-10 gene helps to reduce HIV-1 infection and pathogenic progression

and enables a variety of new therapeutic interventions in the treatment

of HIV disease. The present sequence represents a short tandem repeat

(STR) primer which is used in an example from the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;
primer; probe; tumour suppression; tumour reversion; apoptosis;
virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
                                                                                                                                         Predicting susceptibility to HIV infection or progression useful for selection of therapeutic treatment for persons infected with HIV virus, comprises detecting polymorphism in human interleukin-10 promoter.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 12; DB 3; Length 20; Pred. No. 2.1e+04;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 20 BP; 6 A; 8 C; 3 G; 3 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                    Example 1; Page 12; 40pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GACCGCATAGACTTCTCAGA 20
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O'brien SJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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Best Local Similarity 75.03
Matches 15; Conservative
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Shin HD,
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The invention relates to the isolation of 6327 nucleotide sequences, fragments of at least 15 consecutive nucleotides of these nucleotides, a sequence having at least 80% identity, after optimal alignment, with the nucleotides, or the complement, or corresponding RNA, of the nucleotides. The nucleotides are used as probes or primers for detecting, identifying quantifying and/or amplifying nucleic acids, as in vitro sense and antisense sequences, of nucleotides involved in tumour suppression or reversion, apoptosis and or viral resistance, to produce recombinant polypeptides, and to prepare transgenic animals, as repertamental models. The nucleotides (also vectors containing them and cells containing the vectors), the encoded polypeptides and antibodies of viral infections or diseases characterized by development of tumours or viral infections or diseases characterized by development of tumours or cell degeneration (e.g. Alzheimer's disease or schizophrenia).

Analysis of the expression of the nucleotides can be used for diagnosis also be used to screen for their specific interactive molecules, also permitally useful for treating diseases associated with abnormal
treatment of tumors and viral infection, also related
                                                                               Disclosure; Page 311; 771pp; French
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            expression of the nucleotides.
useful e.g. for treatment of polypeptide and antibodies.
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                                                           Gaps
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                           Score 11.8; DB 10; Length 17;
Pred. No. 2.6e+04;
0; Mismatches 2; Indels (
Sequence 17 BP; 6 A; 5 C; 2 G; 4 T; 0 U; 0 Other;
                           Match 59.0%;
Local Similarity 86.7%;
Les 13; Conservative C
                              Query Match
                                                           Matches
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Human tumour suppression/reversion-related DNA sequence SeqID934. ADI48431 standard; DNA; 17 BP 1 GACCGCATAGACTTC 15 1 GATCACATAGACTIC 15 (first entry) 15-APR-2004 ADI48431; 셤

tumour suppression; tumour reversion; apoptosis; virus resistance; cytostatic; virucide; neuroprotective; nockropic; neuroleptic; probe; primer; PCR; gene chip; antisense; viral disease; tumour; cell degeneration; cancer; Alzheimer's disease; schizophrenia; ds; human. Homo sapiens

WO2003025177-A2.

27-MAR-2003.

17-SEP-2002; 2002WO-IB004523

17-SEP-2001; 2001FR-00011980.

(MOLE-) MOLECULAR ENGINES LAB.

Tuijnder M; relerman A, Amson R,

WPI; 2003-313354/30.

New isolated nucleic acid, useful for treating viral diseases associated with tumors and cell degeneration, also related polypeptides, antibodies and transfected cells.

Disclosure; SEQ ID NO 934; 30pp; French

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                              in the phenomena of tumour suppression, tumour reversion, apoptosis and/or resistance to viruses. The invention may be useful for the development of compounds with a cytostatic, virucide, neuroprotective, nootropic or neuroleptic activity. The DNA sequences may be useful as probes and primers for detecting, indentifying, quantifying and/or amplifying nucleic acid, for example as one component of a gene chip, in vitro as antisense reagents and for production of recombinant pharmaceuticals for prevention may therefore be useful for preparation of pharmaceuticals for prevention and/or treatment of viral diseases that are characterised by development of tumours or cell degeneration, specifically cancer but also Alzheimer's disease and schizophrenia. The present sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The oligos AAQ94315-27 which hybridise to the human-derived cytochrome P450IIC18 gene, esp. to the gene having a point mutation at position 204 in exon 2, can be used as PCR amplification primers which discriminate between the normal and mutated gene, allowing the degree of genetic polymorphism in a patient to be determined. As the gene prod participates in the metabolism of medicines (e.g. tricyclics, benzodiazepines, beta blockers and barbiturates), patients with mutant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human-derived; cytochrome P450IIC18 gene; point mutant; exon 2;
position 204; PCR primer; polymorphism; medicine metabolism; tricyclics;
benzodiazepines; beta blockers; barbiturates; ss.
                invention relates to novel isolated nucleic acid sequences involved
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human cytochrome P450IIC18 exon 2 point mutant 204 PCR primer.
                                                                                                                                                                                                                                                                                                                                                                                          Length 17;
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                                                                                                                                                                                                                                                                                                                                                                                      59.0%; Score 11.8; DB 10;
86.7%; Pred. No. 2.6e+04;
ive 0; Mismatches 2;
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                                                                                                                                                                                                                                                                                                              at ftp.wipo.int/pub/publishedpct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 4; Page 20; 34pp; Japanese.
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Best Local Similarity 86.7
Matches 13, Conservative
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RESULT 21

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trachomatis cryptic plasmid sequence. The primers are used in a method trachomatis cryptic plasmid sequence. The primers are used in a method comprises adding of a nucleic acid analyte for in a sample. The method comprises adding a control nucleic acid analyte cample and two primer pairs, one pair which can amplify a conserved region of the sample nucleic acid and a region of the control nucleic acid to produce fragments (F1, F2) of differing lengths, while the other pair amplifies a second region of the sample nucleic acid to form a sequencing fragments (F1, F2) of the sample nucleic acid to form a sequencing fragment (F3). The method generates a mixture of all 3 fragments if the sample nucleic acid is present but only F2 if it is sometiment in the resultant mixture is analysed for relative amounts of F1 and F2 of the method generates a mixture of F1 and F2 of the method can be used for any infectious organism, e.g. human papilloma virus or characterine the nature of sample nucleic acid. The method can be used for any infectious organism, e.g. human papilloma virus or characted e.g. HIV-1, the disease can be detected and by the amount of amplification product formed, the viral load i.e. the extent of the disease can be assessed. Then by using in the same assay a pair of a paterning leading to a more exert transment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Simultaneous qualitative and quantitative analysis of target nucleic acid - by simultaneous amplification of analyte and control with one primer pair and of sequencing fragment with second primer pair that includes label for immobilisation, especially for HIV-1 detection.
                                                                                                                           Primer; PCR; amplification; gag; qualitative; quantitative; analysis;
infection; diagnosis; detection; serotype; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59.0%; Score 11.8; DB 2; Length 20; 86.7%; Pred. No. 2.7e+04; ive 0; Mismatches 2; Indels
                                                                                     Primer CT1431F for C. trachomatis cryptic plasmid sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Col 8; 18pp; English.
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                                                                                                                                                                                                              Chlamydia trachomatis.
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Best Local Similarity
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                                          25-JAN-1999
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                                                                                                                                                                                              Synthetic.
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  AAV33985;
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Matches
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genes differ in their drug metabolising ability and therefore knowledge of this allows the safe dosage of medicine to be more accurately assessed
                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          beta-adrenergic receptor; brown adipose tissue; probe; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Canine beta 2 and beta 3 adrenergic receptors and coding sequences - useful for identifying specific ligands and (ant)agonists to develop specific treatments for obesity in dogs.
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                                                                                                       Score 11.8; DB 2; Length 18;
Pred. No. 2.6e+04;
0; Mismatches 2; Indels
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                                                              Sequence 18 BP; 5 A; 4 C; 3 G; 6 T; 0 U; 0 Other;
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                                                                                                       Query Match 59.0%;
Best Local Similarity 86.7%;
Matches 13; Conservative 0
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les 13; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lenzen G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       m
                                                                                                                                                                                                                                                                                                                                                                                            AAV30475;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Canine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 22
AAV33985
ID AAV33
XX
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AAV30475

110

AAV30475

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AAV3

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AAV3

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AAV3

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Gaps

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                                                                                                                                                                                                                                                                                                                                        This invention describes a novel method for determining the position of at least one nucleotide (A) within a segment of a target nucleic acid (present in a sample). The method comprises (i) combining the sample with a reaction mixture to synthesize, from the sample, chain-extension products which display the presence of (A) and (ii) evaluating the products. The method is used for diagnosis, e.g. (I) detecting mutations, in human, animal, plant or microbial sequences, particularly medically significant mutations, (II) detecting or identifying microbes, particularly pathogens, or in situ sequencing in histological samples, sepecially archival samples for retrospective analysis. The method makes it possible to sequence segments of a target nucleic acid, even when this is present in its natural concentration in a highly complex sample. It is sultable for any energy and any energy of the concentration in a highly complex sample.
                                                                                                                                                                                                                                                                              Nucleic acid sequencing involving chain extension reaction in presence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; antisense; lung dysfunction; nasal airway dysfunction; antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic; antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy; antisense gene therapy; respiratory; lung; adenosine sensitivity; adenosine receptor; bronchodiation; bronchoconstriction; lung allergy; lung inflammation; respiratory disease; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   for automation; the system represents a way of mimimizing errors caused by contaminants or carried-over nucleic acid; only minimal sample
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               single
                        Detection; target; diagnosis; mutant; human leucocyte antigen typing;
transplantation; pathogen; amplification; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pretreatment is involved and only a single batch of reagent, and sin
vessel, are required. AAZ24114-Z24122 represent primers used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 11.8; DB 3; Length 20; Pred. No. 2.7e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Indels
                                                                                                                                                                                                                           Dunn J, Larson MT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 20 BP; 6 A; 3 C; 5 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                            chain terminator e.g. for detecting mutations.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                           Leushner J, Lacroix J, Hui M,
                                                                                                                                                                                                                                                                                                                      Example 1; Page 9; 18pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human oligonucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABZ91284 standard; DNA; 20 BP
                                                                                                                                             99DE-01017871.
                                                                                                                                                                       98US-00065748.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59.0%;
86.7%;
                                                                                                                                                                                                (VISI-) VISIBLE GENETICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 GCATAGACTICTCAG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCATAAACTTCTGAG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       method of the invention
                                                                                                                                                                                                                                                  WPI; 2000-040351/04.
 Primer CT1431F-Cy5.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                          DE19917871-A1
                                                                                                                                                                       24-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-0CT-2003
                                                                                                                 11-NOV-11999.
                                                                Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABZ91284;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 24
ABZ91284/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonucleotide antisense to the initiation codon, coding region, 5, or 3, end genomic flanking regions, 5, and 3' intron-exon junctions, or regions within 2-10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an antiinflammatory steroid and ubiquinone. A composition of the invention has antiinflammatory, antiallergic, antiasthmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a see in antisense gene therapy. The composition is useful for treating or preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an untifilammatory steroid in a subject, for reducing or depleting levels of, or reducing sensitivity to adenosine, reducing bronchodilation, increasing levels of adenosine receptor, producing bronchodilation, increasing levels of ubiquinone or lung surfactant in a subject's tissue, or treating bronchoconstriction, und subject's tissue, or treating bronchoconstriction, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis; beta-adrenargic agonist; respiratory disease; pulmonary vasconstriction; respiratory distress syndrome; allergic rhinitis; pulmonary hypotremision; emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             respiratory tract inflammation; adenosine sensitivity; lung; cancer; surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Katz E, Pabalan J, Aguilar D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59.0%; Score 11.8; DB 10; 86.7%; Pred. No. 2.7e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 20 BP; 6 A; 4 C; 6 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA486238-derived oligonucleotide SEQ ID 6526.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; SEQ ID NO 6526; 872pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tang L, Shahabuddin S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sandrasagra A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABD27514 standard; DNA; 20 BP.
                                                                                                                                                                                                                           23-APR-2002; 2002WO-US013135.
                                                                                                                                                                                                                                                                                                                                                                                   (EPIG-) EPIGENESIS PHARM INC.
                                                                                                                                                                                                                                                                                                           24-APR-2001; 2001US-0286137P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 CATAGACTTCTCAGA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19 crrácácricícága s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-JUL-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-229219/22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Li Y,
                                                                       WO200285308-A2.
Homo sapiens.
                                                                                                                                                   31-OCT-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ubiquinone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Miller S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABD27514;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nyce JW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABD27514/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 25
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(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-457719/49
                                                                                                                                                                                                                                                                                                                           WO200155214-A2.
                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-MAY-2002
                     24-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABK41518
ઠ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention at cancer and can be anti-sense to the collegonating maken.

The invention also describes a kit, that comprises: (a) a delivery
device, in separate containers, (b) the oligomucleotides, (c)
instructions for adding a carrier and for use of the kit. The composition
of the invention has antiallergic, antiinflammatory, antiasthmatic,
analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
composition comprises oligo and is administered to reduce the production
or availability, or to increase the degradation of the target mRNA or to
reduce the amount of target polypeptide present in the lungs. The
pulmonary obstruction, and/or bronchoconstriction and/or lung
inflammation, allergies and/or surfactant hypoproduction are associated
with a disease or condition such as pulmonary vasconatriction,
inflammation, allergies, asthma, impeded respiration, respiratory
distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
transplantation rejection, pulmonary infections, bronchiis or cancer.
The reduced adenosine content of the anti-sense oligos corresponding to
thymidines present in the target RNA serves to prevent the breakdown of
thymidines present in the target RNA serves to prevent the breakdown of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This invention describes a novel composition (a) a first active agent, comprising oligonuclectides, effective for alleviating bronchoconstriction, respiratory tract inflammation, allergies and reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors, surfactant depletion or hyposecretion, when administered to a mammal. The oligonucleotides are derived from a gene encoding or regulating expression of a target polypeptide associated with lung airway or lung dysfunction or cancer and can be anti-sense to the corresponding mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tissue environment and thereby, to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the oligonucleotides into products that free adenosine into the system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ц
                                                                                                                                                                                                                                                                                                                                                                                                                                             Pharmaceutical composition for treating asthma, has antisense oligonuclectide containing less percentage of adenosine, targeted tnucleic acids associated with lung airway or lung dysfunction, and
                                                                                                                                                                                                                                                                                                                           Aguilar D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59.0%; Score 11.8; DB 11; Length 20; 86.7%; Pred. No. 2.7e+04; ive 0; Mismatches 2; Indels (
                                                                                                                                                                                                                                                                                                                           Pabalan J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 20 BP; 6 A; 4 C; 6 G; 4 T; 0 U; 0 Other;
pulmonary transplantation rejection; ss; primer.
                                                                                                                                                                                                                                                                                                                           Katz E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 15; SEQ ID NO 6526; 763pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      e.g., lung, brain, heart, kidney, etc, prevent any unwanted effects due to it
                                                                                                                                                                                                                                                                                                                                                   ŝ
                                                                                                                                                                                                                                                                                                                         ii Y, Sandrasagra A,
Tang L, Shahabuddin
                                                                                                                                                                                       23-APR-2002; 2002WO-US013143.
                                                                                                                                                                                                                                     24-APR-2001; 2001US-0286036P.
                                                                                                                                                                                                                                                                                (EPIG-) EPIGENESIS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CATAGACTTCTCAGA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTTACACTTCTCAGA 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     bronchodilating agent.
                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-093058/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                              WO200285309-A2
                                                  Homo sapiens
                                                                                                                                         31-OCT-2002
                                                                                                                                                                                                                                                                                                                                Nyce JW,
Miller S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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The invention relates to human asthma-associated gene designated as AAG6. AAG6 is used in the diagnosis, prognosis and treatment of inflammatory or obstructive airway diseases such as asthma, adult respiratory distress syndrome (ARDS), chronic obstructive or pulmonary disease (COPD or COAD), chronic bronchitis, dyspnoea, emphysema and pneumoconiosis. AAG6 is also used in the treatment of eosinophil related disorders such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel polypeptide AAG6 useful for treating an inflammatory or obstructive airways disease, e.g., asthma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    eosinophila, eosinophilic pneumonia, Loffler's syndrome, bronchopulmonary aspergillosis, polyarteritis nodosa and eosinophilic granuloma. AAGE DNA is useful in gene therapy. The present sequence is a PCR primer used for amplifying human AAGE DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; mouse; alpha-catenin; primer; ss; cytostatic; antiinfertility; cadherin-catenin related pathway; heart testis; cancer; gene therapy; cadherin-catenin related disease; specifically dilated cardiomyopathy; cardiomyopathy; male infertility; CTNNA3; PCR; alpha T-catenin.
                                                    Human; asthma-associated gene; AAG6; antiinflammatory; gene therapy; obstructive airway disease; asthma; chronic bronchitis; eosinophila; adult respiratory diserses syndrome, ARDS; dyspnoea; emphysema; COPD; COAD; chronic obstructive or pulmonary disease; pneumoconiosis; eosinophil related disorder; bronchopulmonary aspergillosis; Loffler's syndrome; polyarteritis nodosa; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 11.6; DB 4; Length 19;
Pred. No. 3.4e+04;
0; Mismatches 4; Indels
Human AAG6 DNA exon 1.13 amplifying reverse PCR primer #13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 19 BP; 2 A; 5 C; 6 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human CINNA3 exon-specific upper PCR primer #5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (NOVS ) NOVARTIS AG.
(NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hanley MT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 2; Page 26; 62pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GACCGCATAGACTTCTCA 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-JAN-2001; 2001WO-EP000719.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-JAN-2000; 2000US-00490616
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 58.0
Best Local Similarity 77.8
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Whittaker PA, Jones SJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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AAD11750 standard; DNA; 19 BP

RESULT 26
AAD11750/c
ID AAD11
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AC AAD11

Matches

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8

AAD11750;

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WO200246206-A1
modified base
                                             modified base
                                                                                                                                                                                                                        Popoff I,
                                                                                                                                                                                                                                                                                                       hepatitis
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ADK78853/c
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                                                                                                                                                                                                                                           The invention relates to human and mouse alpha-catenin polypeptides and their associated polynucleotides. The polypeptides and related antibodies set useful for modularing the cadherin-catenin related pathway in selected organs, such as the heart and testis. The nucleic acids and the antibodies are useful in the diagnosis and/or prediction of the likelihood of developing cadherin-catenin related diseases. The nucleic acids may also be used to predict the likelihood of developing cancer or in diagnosing cancer, and in gene therapy. The polypeptide, the nucleic acid or the antibody is useful in manufacturing a medicament for treating cadherin-catenin related diseases, such as cancer, cardiomyopathy, specifically dilated cardiomyopathy, and male infertility. Sequences ABK41510-ABK4159 represent PCK primers used to amplify DNA encoding human and mouse alpha-catenin polypeptides, including the CTNNA3 gene
                                                                                                                                                                          New alpha catenin polypeptides and polynucleotides encoding them, useful for predicting, diagnosing or treating cadherin-catenin related diseases, particularly cardiomyopathies, cancer and male infertility.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human damage specific DNA binding protein 1 antisense oligonucleotide #5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antisense; cytostatic; hepatotrophic; antiinflammatory; virucide; Damage-specific DNA-binding protein 1; p127; cancer; human; 88; hyperproliferative disorder; haematopoietic cancer; hepatitis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             58.0%; Score 11.6; DB 6; Length 20; 77.8%; Pred. No. 3.4e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mod_base= OTHER
/note= "OTHER= phosphorothioate backbone"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Indels
                                                                                                                              Vanpoucke G;
                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 20 BP; 5 A; 5 C; 5 G; 5 T; 0 U; 0 Other;
                                                                                                       (VLAA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                              Janssens B,
                                                                                                                                                                                                                                                                                                                                                                                                  which encodes human alpha T-catenin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                        Example, Page 35; 132pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GACCGCATAGACTTCTCA 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 GACTGAACAGGCTTCTCA 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABS59713 standard; DNA; 20 BP.
                                               28-JUN-2001; 2001WO-EP007392
                                                                    12-JUL-2000; 2000EP-00202472
14-JUL-2000; 2000US-0218309P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 77.8 les 14; Conservative
                                                                                                                                Goossens S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            *tag=
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                                                                                                                                                    WPI; 2002-171717/22.
 WO200204636-A1.
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modified_base
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-NOV-2002
                        17-JAN-2002
                                                                                                                              Van Roy F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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This invention relates to a novel antisense compound 8 to 50 nucleobases in length targeted to nucleic acid molecule encoding Damage-specific DNA-binding protein 1, p127 where the antisense compound specifically chybridises with and inhibits expression of the damage specific DNA-binding protein-1 gene. The compounds of the invention may be used in binding protein 1, p127. The antisense compounds of the invention are consecuted for inhibiting the expression of damage specific DNA-binding protein 1, p127 in cells or itssues and are also useful for treating an animal having a disease or condition associated with expression of p127, such as a hyperproliferative disorder (e.g., cancer such as breast, skin, such as a hyperproliferative disorder (e.g., cancer such as breast, skin, such as a hyperproliferative disorder (e.g., cancer such as breast, skin, such as a hyperproliferative disorder (e.g., cancer such as breast, skin, carpression of p127. All antisense oligonucleotides of the invention are chimeric oligonucleotides (gapmers) on ucleotides in length, composed of chimeric oligonucleotides (spaners) 20 nucleotides in length, composed of 2'-methoxyethyl (2'-MOB) nucleotides. The internucleoside (backbone) linkages are phosphorothioate (P=S) throughout the oligonucleotide and all cytidine residues are 5-methylcytidines. The present sequence represents a damage-specific DNA binding protein 1, p127 contine of the invention contines and page-specific DNA binding protein 1, p127 contines DNA page-specific DNA page-spe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel antisense compound targeted to nucleic acid molecule encoding Damage-specific DNA-binding protein 1, p127, useful for treating animal having disease associated with the protein such as liver cancer, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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0
                                              /mod_base= OTHER
/note= "OTHER= 2'-O-methoxyethyl nucleotide"
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/mod_base= OTHER
/note= "OTHER= 2'-0-methoxyethyl nucleotide"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Page 89; Claim 3; 121pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GACCGCATAGACTTCTCA 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-DEC-2001; 2001WO-US046485.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-DEC-2000; 2000US-00731457.
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/*tag= b
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                                                                                                  not\overline{e} = "C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ISIS-) ISIS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-599454/64.
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Best Local Similarity
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The present invention relates to an antisense compound targeted to a nucleic acid molecule encoding Nav1.3, where the antisense compound specifically hybridizes with and inhibits the expression of Nav1.3. The compound and composition are useful for treating a disease or condition associated with Nav1.3, e.g. pain including but not limited to neuropathic pain, post-herpetic neuralgia, chronic pain, lower back pain, adiabetic neuropathy ringeminal neuropathy, arthritic pain, acute pain, pain from burns, migraine headache, cluster headache, mild-to-moderate cheadache; seizure disorder such as childhood saizure disorder, including but not limited to neonatal or infantile epilepsy; or ataxia. The present sequence represents a chimeric phosphorchhoate oligonucleotide with 2'MOE wings and a deoxy gap. Used during the antisense inhibition of human Nav1.3 expression, the oligonucleotides are designed to target
                                                                                                                                                                                                                              New antisense compound targeted to a nucleic acid molecule encoding Nav1.3, useful for useful for treating a disease or condition associated with Nav1.3, e.g. pain, seizure disorder such as childhood seizure disorder, or ataxia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Navl.3; Analgesic; Nootropic; Neuroprotective; post-herpetic neuralgia;
diabetic neuropathy; arthritic pain; migraine headache;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chimeric phosphorothicate oligonucleotide to target Navl.3 #6186.
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Pred. No. 3.4e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 20 BP; 7 A; 4 C; 3 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                       Claim 4; SEQ ID NO 5789; 417pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GACCGCATAGACTTCTCA 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                infantile epilepsy; ataxia; ss
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                                              14-AUG-2002; 2002US-0403416P.
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  14-AUG-2003; 2003WO-US025465
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 77.8%;
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19 GACTGCTTAGAGTTTTCA
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                                                                                             (PHAA ) PHARMACIA CORP
                                                                                                                                                                                          WPI; 2004-203785/19.
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                                                                                                                                           Roberds SL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      associated with Navl.3, e.g. pain including but not limited to neuropathic pain, post-herpetic neuralgia, chronic pain, lower back pain, diabetic neuropathy, trigeminal neuropathy, arthritic pain, acute pain, pain from burns, migraine headache, cluster headache, mild-to-moderate headache; seizure disorder such as childhood seizure disorder, including but not limited to neonatal or infantile epilepsy; or ataxia. The present sequence represents a chimeric phosphorothioate oligonucleotide with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New antisense compound targeted to a nucleic acid molecule encoding Nav1.3, useful for useful for treating a disease or condition associated with Nav1.3, e.g. pain, seizure disorder such as childhood seizure disorder, or ataxia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to an antisense compound targeted to a nucleic acid molecule encoding Nav1.3, where the antisense compound specifically hybridizes with and inhibits the expression of Nav1.3. The compound and composition are useful for treating a disease or condition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Navl.3; Analgesic; Nootropic; Neuroprotective; post-herpetic neuralgia; diabetic neuropathy; arthritic pain; migraine headache; infantile epilepsy; ataxia; 88.
Navl.3; Analgesic; Nootropic; Neuroprotective; post-herpetic neuralgia; diabetic neuropathy; arthritic pain; migraine headache; infantile epilepsy; ataxia; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2'MOE wings and a deoxy gap. Used during the antisense inhibition of human Nav1.3 expression, the oligonucleotides are designed to target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chimeric phosphorothioate oligonucleotide to target Navl.3 #5789.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58.0%; Score 11.6; DB 12; Length 20; 77.8%; Pred. No. 3.4e+04; Indels ive 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 20 BP; 7 A; 5 C; 3 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      different regions of the human Nav1.3 RNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 4; SEQ ID NO 6187; 417pp; English.
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                                                                                                                                                                                                                                                                                    14-AUG-2002; 2002US-0403416P.
                                                                                                                                                                                                                                        14-AUG-2003; 2003WO-US025465.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GACTGCTTAGAGTTTTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                 (PHAA ) PHARMACIA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2004-203785/19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
                                                                                                                                           WO2004016754-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO2004016754-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-MAY-2004
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                                                                                                                                                                                          26-FEB-2004
                                                                                                                                                                                                                                                                                                                                                                                    Roberds SL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                  Synthetic
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Matches

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Gaps

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Length 20; Indels

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                                                                                                                                     The present invention relates to an antisense compound targeted to a nucleic acid molecule encoding Navi.3, where the antisense compound specifically hybridizes with and inhibits the expression of Navi.3. The compound and composition are useful for treating a disease or condition associated with Navi.3, e.g. pain including but not limited to neuropathic pain, post-herpetic neuralia, chronic pain, lower back pain, diabetic neuropathy, trigeminal neuropathy, arthritic pain, acute pain, pain from burns, migraine headache, cluster headache, mild-to-moderate but not limited to neonatal or infantile epilepsy; or ataxia. The present sequence represents a chimeric phosphorothioate oligonucleotide with 2. MoE wings and a deoxy gap. Used during the antisense inhibition of human Navi.3 expression, the oligonucleotides are designed to target different regions of the human Navi.3 RNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition; gene expression; downregulation; interleukin-5; IL-5; ICAM-1; intercellular adhesion molecule; rel A; tumour necrosis factor; TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene; translocation; chronic myelogenous leukaemia; CML; cancer; Philadelphia chromosome; inflammation; attoke; restenosis; transplant rejection; rheumatoid arthritis; psoriasis; myocardial infarction; stroke; restenosis; transplant rejection; rheumatoid arthritis; psoriasis; myocardial ischaemia; Kawasaki disease; septic shock; HIV; human immunodeficiency virus; acquired immune deficiency syndrome; AIDS;
... antibense compound targeted to a nucleic acid molecule encoding Navl.3, useful for useful for treating a disease or condition associated with Navl.3, e.g. pain, seizure disorder such as childhood seizure disorder, or ataxia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human relA hammerhead ribozyme target sequence (nt. position 1704).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 11.6; DB 12; Length 20; Pred. No. 3.4e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 20 BP; 7 A; 4 C; 4 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                         Claim 4; SEQ ID NO 6186; 417pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GACCGCATAGACTTCTCA 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18 GACTGCTTAGAGTTTTCA 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             В
В
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94US-00218934.
94US-00222795.
94US-00227958.
94US-00228041.
94US-00245736.
94US-00245736.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 77.8%;
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95WO-IB000156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAT55168 standard; RNA; 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-APR-1994;
18-MAY-1994;
06-JUL-1994;
15-AUG-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-FEB-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9523225-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-FEB-1994;
29-MAR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-MAR-2003
22-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-APR-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAT55168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 32
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The present sequence represents a preferred target sequence for an enzymatic nucleic acid (i.e. a ribozyme) which cleaves relA mRNA at the enzymatic nucleide base position indicated in the DE line. The relA gene product is a subunit of the transcriptional regulator NF-kappaB and is implicated specifically in the induction of inflammatory responses. Regions of the contrain potential hammerhead and hairpin ribozyme cleavage sites were identified by computer analysis. Ribozymes directed against these mRNA sequences by computer analysis. Ribozymes directed against these mRNA sequences by computer analysis and hairpin ribozyme cleavage sites were identified by computer analysis in the ribozymes are designed to cleave their contrain unclease resistance. The ribozymes are designed to cleave the target sequences and thereby inhibit relA expression, making them potentially useful for treating rheumatoid arthritis, restenosis and asthma as well as for increasing tolerance to transplanted tissues. The potential immunosuppressive properties of a thosyme that cleaves relA mRNA means that uses are limited to local delivery, acute indications or ex vivo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                     o DT, Chowrira B, Direnzo A, Draper KG, Dudycz LW; Karpeisky A, Kisich K, Matulic-Adamic J, Mcswiggen JA; Karpeisky B, Kaigleman L, Sullivan SM, Sweedler D, Thompson JD; Usman N, Wincott FE, Woolf T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ribozymes having modified bases and methods for producing them - for use in inhibiting disease related genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Enzymatic nucleic acid; nuclear factor kappa B; NFKB; inozyme; zinzyme; G-cleaver; amberzyme; cancer; REL-A activity; breast cancer; human; lung cancer; prostate cancer; colorectal cancer; brain cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           treatment. (Updated on 25-MAR-2003 to correct PI field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NFKB sub-unit modulating amberzyme substrate #225.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 15 BP; 3 A; 5 C; 3 G; 0 T; 4 U; 0 Other,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 2; Page 229; 407pp; English.
            94US-00292620.
94US-00293520.
94US-00303030.
94US-00311486.
94US-00311449.
94US-00316771.
94US-0031993.
94US-00334847.
94US-00334847.
94US-00334847.
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94US-00291433
                                                                                                                                                                                                                                                                     94US-00363233
                                                                                                                                                                                                                                                                                    95US-00380734
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Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                         (RIBO-) RIBOZYME PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACA09062 standard; RNA; 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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1 AUGGACUUCUCAG 13
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                                                                                     23-SEP-1994;
                                                                                                                                                                                                                                                                                    30-JAN-1995;
                                                                    08-SEP-1994;
                                                                                                                                                                                               04-NOV-1994
                                                                                                                        28-SEP-1994
                                                                                                                                                           07-OCT-1994
                                                                                                                                                                              11~OCT-1994
                                                                                                                                                                                                                 10-NOV-1994
                                                                                                                                                                                                                                                     16-DEC-1994
                                                                                                                                                                                                                                                                                                                                                         Stinchcomb
                                                                                                                                                                                                                                                                                                                                                                           Grimm S,
Modak A,
Tracz D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACA09062;
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tumour suppression; tumour reversion; apoptosis; virus resistance; cytostatic; virucide; neuroprotective; nootropic; neuroleptic; probe; primer; PCR; gene chip; antisense; viral disease; tumour; cell degeneration; cancer; Alzheimer's disease; schizophrenia; ds; human.

WO2003025177-A2.

27-MAR-2003.

Homo sapiens.

Human tumour suppression/reversion-related DNA sequence SeqID288

(first entry)

15-APR-2004

ADI47785;

ADI47785 standard; DNA; 17 BP

RESULT 34

ADI47785/

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Novel enzymatic nucleic acid molecules which down regulates expression of a sequence encoding a subunit of nuclear factor kappa B useful for treating cancer, inflammatory disorders and autoimmune diseases.
oesophageal cancer; stomach cancer; bladder cancer; pancreatic cancer; cervical cancer; head and neck cancer; ovarian cancer; melanoma; lymphoma; glioma; multidrug resistant cancer; RELA-specific inhibitor; chemotherapy; paclitaxel; docetaxel; cisplatin; methotraxate; cyclophosphanide; doxorubin; fluorouracil carboplatin; edatexate; gemcitabine; radiation therapy; inflammatory disease; asthma; diabetes; rheumatorid arthritis; restenosis; Crohn's disease; obesity; ischaemia; gene therapy; autoimmune disease; lupus; multiple sclerosis; sepsis; transplant/graft rejection; reperfusion injury; glomerulonephritis; allergic airway inflammation; inflammatory bowel disease; infection; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 3; Page 55; 72pp; English.
                                                                                                                                                                                                                                                   94US-00245466.
94US-00291932.
96US-00777916.
                                                                                                                                                                                                                                                                                                                                                     Mcswiggen J,
                                                                                                                                                                                                               23-MAY-2001; 2001US-00864785
                                                                                                                                                                                                                                                                                                   STINCHCOMB D T.
                                                                                                                                                                                                                                                                                                                                                                            VPI; 2003-340953/32.
                                                                                                                                                                                                                                                                                                                             DRAPER K G.
                                                                                                                                                                                                                                                                                                                 MCSWIGGEN
                                                                                                                                                                US2002177568-A1.
                                                                                                                                                                                                                                                                                                                                                     Stinchcomb DT,
                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                      18-MAY-1994;
                                                                                                                                                                                                                                                               15-AUG-1994;
23-DEC-1996;
                                                                                                                                                                                                                                        07-DEC-1992;
                                                                                                                                                                                        28-NOV-2002
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                                                                                                                                                                                                                                                                                                                             DRAP/)
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Draper KG;

The invention describes an enzymatic nucleic acid molecule (I) which down regulates expression of a sequence encoding a subunit of nuclear factor regulates expression of a sequence encoding a subunit of nuclear factor configuration. The enzymatic nucleic acid molecule is adapted to treat cancer and is useful for down-regulating REL-A activity in a cell, for creating a patient having a condition associated with the level of REL-A. (I) is useful for cleaving RNA comprising a sequence of REL-A gene, in the presence of a divalent cation, especially MG^2+. The enzymatic and antisense nucleic acid molecules are useful for treating breast, lung, prostate, colorectal, brain, oesophageal, stomach, bladder, pancreatic, cervical, head and neck, ovarian cancer, melanoma, lymphoma, glioma or multidrug resistant cancer. The method involves use of other drug chemotherapy including paclitaxel, docetaxel, cisplatin, methotrexate, cyclophosphamide, doxorubin, fluorouracil carboplatin, edatrexate, cyclophosphamide, doxorubin, fluorouracil carboplatin, edatrexate, caid molecules are also useful for treating inflammatory disease such as chemiatod, arthritis, restenosis, asthma, Crohn's disease, diabetes, colorin, acon thorse and injury autoinmune disease, lupus, multiple sclerosis, transplant/graft coloring control. infection. This sequence represents the substrate of a novel enzymatic rejection, gene therapy applications, ischaemia/reperfusion injury (central nervous system (CNS) and myocardial), glomerulonephritis, sepsis, allergic airway inflammation, inflammatory bowel disease or nucleic acid molecule

Sequence 17 BP; 4 A; S C; 4 G; 0 T; 4 U; 0 Other;

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Score 11.4; DB 8; Length 17; Pred. No. 4.3e+04; 4; Mismatches 1; Indels
     57.0%;
61.5%;
                                                        CATAGACTTCTCA 18
                 Similarity 61.5
8; Conservative
                                                         9
     Query Match
Best Local
                              Matches
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CAUGGACUUCUCA 17

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Gaps

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This invention relates to novel isolated nucleic acid sequences involved in the phenomena of tumour suppression, tumour reversion, apoptosis and/or resistance to viruses. The invention may be useful for the development of compounds with a cytostatic, virucide, neuroprotective, nootropic or neuroleptic activity. The DNA sequences may be useful as probes and primers for detecting, indentifying, quantifying and/or amplifying nucleic acid, for example as one component of a gene chip, in viro as antisense reagents and for production of recombinant polypeptides. The invention may therefore be useful for preparation of pharmaceuticals for prevention and/or treatment of riral diseases that are characterised by development of tumours or cell degeneration, specifically cancer but also Alzehimer's disease and schizophrenia. The present sequence data for this patent did not form part of the invention.

Note: The sequence data for this patent did not form part of the printed Note: The sequence data for this patent did not form part of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated nucleic acid, useful for treating viral diseases associated with tumors and cell degeneration, also related polypeptides, antibodies and transfected cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57.0%; Score 11.4; DB 10; 92.3%; Pred. No. 4.3e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 17 BP; 6 A; 4 C; 3 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ftp.wipo.int/pub/publishedpct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; SEQ ID NO 288; 30pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                   Tuijnder M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BP.
                                                                                                                                                                                                                                                                                                                                                                                (MOLE-) MOLECULAR ENGINES LAB
                                                                                                                                                                                                                                                                                                            17-SEP-2002; 2002WO-IB004523.
                                                                                                                                                                                                                                                                                                                                             17-SEP-2001; 2001FR-00011980.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAA83653 standard; DNA; 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-DEC-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 92.3*
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 TAGACTICICAGA 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-313354/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      specification,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAA83653;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 35
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8
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WPI; 2000-412314/35.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        sapiens
                                                                                                                                                                                                                                                                                                      10-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-MAY-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Robbins JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                 RESULT 37
AAH58814/c
                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo
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                                                                                                                                                                                                                                                                                                                                                           ô
                                                                                                                                                                                                                                        The present invention relates to a hairpin or hammerhead ribozyme, designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase other than cell-cycle dependent kinases CDK1. PCKN and Cyclin B1.
Representative examples of ribozyme recognition sites are given in AAA86745. The ribozyme of the invention is useful for inhibiting restencies by introduction of the ribozyme into cells. The ribozyme is resistant to endonuclease activity and hence is efficient in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.
                          Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.
                                                                                                                                                                                 New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1, PCNA and Cyclin B1.
                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                                                                                                       57.0%; Score 11.4; DB 3; Length 19; 92.3%; Pred. No. 4.3e+04; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                        Sequence 19 BP; 6 A; 3 C; 5 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Barber JR, Robbins JM;
                                                                                                                                                    Robbins JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cdk-we-hu ribozyme binding site #127.
          cdk-we-hu ribozyme binding site #128
                                                                                                                                                                                                                         Disclosure; Page 65; 109pp; English.
                                                                                                                                                    Barber JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                         BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99WO-US028772
                                                                                                                 98US-0110954P
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                                                                                                                                                                                                                                                                                                                                                                                                                                        AAA83652 standard; DNA; 19
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                                                                                                                                                                                                                                                                                                      restenosis treatment
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                                                                                                                                                    Tritz R, Welch PJ,
                                                                                                                                                                    WPI; 2000-412314/35
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                                                                                                                                  (IMMO-) IMMOSOL INC
                                                             WO200032765-A2
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                                             Mammalia
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Human, ribozyme therapy, hairpin ribozyme; hammerhead ribozyme; recognition site; target; ribozyme binding site; eye disease; vulnerary; proliferative disease; skin disease; psoriasis; diabetic retinopathy; cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP; matrix metalloproteinase; growth factor; reductase; scarring; cytostatic; antipsoriatic; dermatological; antiesborrheic; antidiabetic; virucide; antisickling; ophthalmological; scaraclytic; gene therapy; viral wart; atopic dermatitis; actinic keratosis; squamous cell carcinoma; basal cell carcinoma; seborrheic wart; vitreoretinopathy; scar;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Treating proliferative skin or eye diseases and scarring, using ribozymes that cleave RNA encoding cytokines involved in inflammation, matrix metalloproteinases, growth factors and cell-cycle dependent kinases.
                                                                                                                                                                                                                                            The present invention relates to a hairpin or hammerhead ribozyme, designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase other than cell-cycle dependent kinases CDR1, FCNA and Cyclin B1.

Representative examples of ribozyme recognition sites are given in AAA82415 to AAA86787. The ribozyme of the invention is useful for inhibiting restenosis by incroduction of the ribozyme into cells. The ribozyme is resistant to endonuclease activity and hence is efficient in restenosis treatment
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New hairpin and hammerhead ribozyme for inhibiting restenosis, cleave RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1, PCNA and Cyclin B1.
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0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seguence 19 BP; 7 A; 2 C; 5 G; 5 T; 0 U; 0 Other;
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                                                                                                                                                                           Disclosure; Page 65; 109pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAH58814 standard; DNA; 19 BP.
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c skin or eye disease and scarring. The method involves administering a ribozyme (I) which cleaves RNA encoding a cytokine involved in inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle dependent kinase, growth factor or a reductase, or administering a nucleic acid molecule (II) comprising a promoter operably linked to a nucleic acid segment encoding (I). (I) can have antipsoriatic, dermatological, vulnerary, keratolytic and virucide activities, and cleaves RNA encoding cytokine involved in inflammation. (I) can be used in gene therapy. (I) and (II) are useful for treating proliferative skin diseases such as psoriasis, atopic dermaticis, actinic keratosis, squamous or basal cell carcinoma and viral or seborrheic wart. They can also be used for treating proliferative eye diseases such as diabbetic retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of prematurity and retinal detachment, and for treating and preventing such as keloid, adhesion and hypertrophic or hypertrophic burn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                scar, AAH57577 to AAH62099 represent sequences used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             exemplification of the present invention
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Sequence 19 BP; 7 A; 2 C; 5 G; 5 T; 0 U; 0 Other;

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Gaps
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0
Score 11.4; DB 5; Length 19;
Pred. No. 4.3e+04;
0; Mismatches 1; Indels
   57.0%;
92.3%;
                Best Local Similarity 92.3
Matches 12; Conservative
    Query Match
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5 GCATAGACTICIC 17 15 GCATATACTICTC 3 셤 ઠે

AAH58815; RESULT 38

Cdk-we-hu ribozyme binding site SEQ ID NO:1239. AAH58815 standard; DNA; 19 BP 10-SEP-2001 (first entry)

Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme; recognition site; target; ribozyme binding site; eye disease; vulnerary; proliferative disease; skin disease; psoriasis; diabetic retinopathy; cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP; matrix metalloproteinase; growth factor; reductase; scarring; cytostatic; antipsoriatic; dermatological; antiseborrheic; antidiabetic; virucide; antisickling; ophthalmological; keracolytic; gene therapy; viral wart; atopic dermatitis; actinic keratosis; squamous cell carcinoma; basaal cell carcinoma; seborrheic wart; vitreoretinopathy; scar; sickle cell retinopathy; ss.

Homo sapiens Synthetic.

WO200130362-A2.

03-MAY-2001.

26-OCT-1999; 99US-0161532P. 26-OCT-2000; 2000WO-US029500

(IMMU-) IMMUSOL INC.

Robbins JM, Tritz R;

WPI; 2001-300427/31.

Treating proliferative skin or eye diseases and scarring, using ribozymes that cleave RNA encoding cytokines involved in inflammation, matrix metalloproteinases, growth factors and cell-cycle dependent kinases.

Example 1; Page 162; 408pp; English

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The present invention describes a method for treating a proliferative skin or eye disease and scarring. The method involves administering a ribozyme (1) which cleaves RNA encoding a cytokine involved in inflammation, matrix metalloproteinase (WMP), cyclin, cell-cycle dependent kinase, growth factor or a reductase, or administering a nucleic acid molecule (II) comprising a promoter operably linked to a nucleic acid segment encoding (I). (I) can have antipsoriatic, dermatological, cytostatic, antiseborrheic, antidiabetic, antisickling, ophthalmological, vulnerary, keratolytic and virucide activities, and cleaves RNA encoding cytokine involved in inflammation. (I) can be used in gene therapy. (I) and (II) are useful for treating proliferative skin diseases such as psoriasis, atopic dermaticis, actinic keratosis, diseases uch as psoriasis, atopic dermaticis, actinic keratosis.

Company, virreoretinopathy, sickle cell retinopathy of prematurity and retinal detachment, and for treating and preventing proliferative eye diseases such as diabetic retinopathy, virreoretinopathy, sickle cell retinopathy, retinopathy of prematurity and retinal detachment, and for treating and preventing carring such as keloid, adhesion and hypertrophic or hypertrophic burn securing such as keloid, adhesion and species used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    exemplification of the present invention
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Sequence 19 BP; 6 A; 3 C; 5 G; 5 T; 0 U; 0 Other;

Gaps ö Score 11.4; DB 5; Length 19; Pred. No. 4.3e+04; 0; Mismatches 1; Indels 57.0%; 12; Conservative Local Similarity Query Match Matches

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5 GCATAGACTICIC 17 13 GCATATACTTCTC 1 g ઠે

Anti-KCNH1 siRNA SEQ ID NO:1588. 멺. ADQ61886 standard; RNA; 19 09-SEP-2004 ADQ61886; RESULT 39 ADQ61886/

ss; siRNA; gene silencing; Bcl-2; optimised; short interfering RNA; RNA interference. 14-NOV-2003; 2003WO-US036787. WO2004045543-A2. 03-JUN-2004 Synthetic.

14-NOV-2002; 2002US-0426137P. 10-SEP-2003; 2003US-0502050P. (DHAR-) DHARMACON INC.

Devin L, William M, Stephen Anastasia K, Angela R,

WPI; 2004-420527/39.

Selecting siRNA by selecting an siRNA molecule of 19-25 nucleoside bases by selecting a target gene and measuring the functionality of the nucleotide sequences that are complementary to a stretch of nucleotides of the target sequence.

Example 12; SEQ ID NO 1588; 199pp; English.

The invention relates to a novel method for selecting siRNA (short interfering RNA) comprising selecting an siRNA molecule of 19-25 nucleoside bases by selecting a target gene and measuring the functionality of sequences of 19-25 nucleotides in length that are

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comprises a hairpin. The siRNA molecule comprises between 18 and 30 base comprises a hairpin. The siRNA molecule comprises a between the functionality is dependent upon non-target specific criteria. Also claimed are methods for gene-silencing, developing an siRNA algorithm for selecting siRNA, selecting an siRNA with improved functionality, selecting siRNA, selecting an siRNA molecule comprises a sequence substantially similar to a sequence consisting of GGGAGAUAGUAGAAGUA, GAAGUACAUCAGUAUAAG; GUACGACACACCGGGAGAUA, GGGACAUCGUUGAAUGA, GAAGUACAUCCAUGAAGUA, GAAGUACAUCCAUUGA, UGAAGACCUCGUUGAAUU, GAGAUAGUAGAAGUACA, GGAGAUAGUAGAAGUACA, The siRNA molecule comprises a sense strand and an anti-sense strand. The siRNA molecule comprises a hairpin. The siRNA molecule comprises between 18 and 30 base comprises. The kit comprises at least two siRNA, comprising a first optimised siRNA. The method is useful in selecting siRNA for generating a gene silencing reagent. The present sequence is used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 19 BP; 6 A; 2 C; 5 G; 0 T; 6 U; 0 Other;
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ö Gaps ö 57.0%; Score 11.4; DB 12; Length 19; 92.3%; Pred. No. 4.3e+04; ive 0; Mismatches 1; Indels (12; Conservative Best Local Similarity Query Match Matches

7 ATAGACTICICAG 19 14 ATAGACCTCTCAG 2 쉽 ઠે

AAX77133 standard; DNA; 20 BP 03-AUG-1999 (first entry) PCR primer 92-5' AAX77133;

Cellular senescence; modulator; GC6 gene; senescent gene expression; pGC6; human; PCR primer; ss

Synthetic.

W09925878-A2

27-MAY-1999

98WO-US024996 19-NOV-1998;

97US-00974180 19-NOV-1997;

(GERO-) GERON CORP.

Funk W;

WPI; 1999-347496/29.

New human GC6 gene, useful for identifying agents for treating diseases and/or conditions associated with cell senescence.

Example 5; Page 74; 79pp; English.

The invention relates to methods for modulating and identifying cellular senescence. Recombinant expression vectors comprising a recombinant polynucleotide corresponding to a polynucleotide in a human GC6 gene, are useful for altering senescent gene expression. The vectors and host cells comprising the vectors are useful for indentifying agents that prevent or modulate senescent gene expression. The polynucleotides are useful for producing the protein, 9GC6 and nucleic acid derivatives. The proteins encoded are useful for raising antibodies specific for pGC6, which are useful for a constant of the proteins of the characterization of the polynucleotides enable

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the identification of therapeutic agents that identify and distinguish between young and senescent cells. This enables treatment of aging diseases induced or exacerbated by cellular senescence
                                                                                                         Sequence 20 BP; 7 A; 6 C; 4 G; 3 T; 0 U; 0 Other;
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US-09-081-646-202

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US-09-081-646-202

US-09-081-646-203

US-09-124-398-5

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US-09-113-309-6

US-08-1108A-6

US-09-866-108A-6

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Patent No. 5401629
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204, App
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Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-038-637-113

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US-08-229-150-4

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US-09-696-791-1239

US-09-128-4269-113

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US-09-188-428-3744

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                                                                COMPUTER: U.S.A.

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ZIP: 92008

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch disk, 1.44 Mb

COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows NT
SOFTWARE: Microsoft Word 97

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/106,038A

FILING DATE: June 26, 1998

CLASSIFICATION NUMBER: S14

ATTORNEY/AGENT INFORMATION:
NAME: Laurel Spear Bernstein
REGISTRATION NUMBER: 37,280

REGISTRATION NUMBER: RTS-0004

TELEFRONE: (760) 931-9200

TELEFRA: (760) 931-9200

TELEFRA: (760) 603-3820

INPORMATION FOR SEQ ID NO: 75:
SEQUENCE CHARACTERISTICS:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/922,723A
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: D.J. Mills
REGISTRATION NUMBER: 34506
REFERENCE/DOCKET NUMBER: 7170;
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703 684 1111
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
2292 Faraday Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 CGCATAGACTTCTCAGA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18 cecesagrerrereas 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                Carlsbad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
TOPOLOGY: lin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-106-038A-75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 4
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                                                                                                                                                                                                          Sequence 2812, Application US/09198452A

Patent No. 6559294

GENERAL INFORMATION:
APPLICANT: GTIffala, R.
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, preverittle Reference: 9710-003-999
TITLE OF INVENTION: and treatment of infection
TITLE REFERENCE: 9710-003-999
CURRENT APPLICATION NUMBER: US/09/198,452A

CURRENT PILING DATE: 1998-11-24

NUMBER OF SEQ ID NOS: 6849

SEQ ID NO 2812

LENGTH: 20
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US-10-007-010-48/C
; Sequence 48, Application US/10007010
; Patent No. 6828151
; GENERAL INFORMATION:
; APPLICAMT: ALexander H. Borchers
; APPLICAMT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF HCK EXPRESSION
; TITLE OF INVENTION: ANTISENSE WOULATION OF HCK EXPRESSION
; CURRENT APPLICATION NUMBER: US/10/007,010
; CURRENT PILING DATE: 2001-12-04
; NUMBER OF SEQ 1D NOS: 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69.0%; Score 13.8; DB 4; Length 20; 88.2%; Pred. No. 6e+02; cive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 66.0%; Score 13.2; DB 4; Length 20; Best Local Similarity 83.3%; Pred. No. 1.3e+03; Matches 15; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Antisense Oligonucleotide US-10-007-010-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 ACCGCATAGACTTCTCAG 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Chlamydia pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GACCGCATAGACTTCTC 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 GACCGCATAAACTTATC 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 88.2
Matches 15, Conservative
                                                                                                                                                                       RESULT 1
US-09-198-452A-2812
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LENGTH: 20
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TITLE OF INVENTION: ELEVEN HIGHLY INFORMATIVE
TITLE OF INVENTION: REPEAT FOLYMORPHIC DNA MARKERS
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lowe, Price, LeBlanc & Becker
STREET: Suite 300, 99 Canal Center Plaza
CITY: Alexandria
STATE: Virginia
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COMPUTER READABLE FORM:

MEDIUM TYPE: Disketer

COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows 95

SOFTWARE: FASLSEQ for Windows Version 2.0b

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/038,637

FILING DATE: 10-MAR-1998

FILING DATE: 28-DEC-1995

APPLICATION NUMBER: 08/579,233

FILING DATE: 12-NOV-1993

ATTORNY DATE: 12-NOV-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: DOS Text File
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/952,277A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: D.J. Mills
REGISTRATION NUMBER: 34506
                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
CMBDIUM TYPE: Floppy disk
CMBUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 703 64 1111
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) US-07-952-277A-60
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STRANDEDNESS: single
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                                                                                                                                                                                                                  Query Match 60.0%; Score 12; DB 1; Length 20; Best Local Similarity 75.0%; Pred. No. 5.5e+03; Matches 15; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 60, Application US/07799828C

| Patent No. 5378602
| Patent No. 5378602
| Patent No. F. Carl R. Merril and APPLICANT: Mihael H. Polymeropoulos
| TITLE OF INVENTION: TWENTY SEVEN HIGHLY INFORMATIVE
| TITLE OF INVENTION: POLYMORPHIC DNA MARKERS
| TITLE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Drs. Mihael H. Polymeropoulos APPLICANT: and Carl R. Merril
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: DOS Text File
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/799,828C
FILING DATE: 19911127
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: D.J. Mills
REGISTRATION NUMBER: 34,506
REFERENCE/DOCKET NUMBER: 717081A
TELECHONIOI (INFORMATION: TELECHONIOI (INFORMATION: TELECHONIOI (INFORMATION: SEQUENCE CHARACTERISTICS: SEQUENCE CHARACTERISTICS:
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COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Sequence 60, Application US/07952277A
Patent No. 5861504
GENERAL INFORMATION:
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          TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
WOLECULE TYPE: DNA (genomic)
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MOLECULE TYPE: DNA (genomic)
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Best Local Similarity 75.0°
Matches 15; Conservative
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STRANDEDNESS: single
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US-07-799-828C-60
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Sequence 113, Application US/09038637
Sequence 113, Application US/09038637
Sequence 113, ADDRESSEE: Figh & Richardson P.C.
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Query Match 60.0%; Score 12; DB 2; Length 20; Best Local Similarity 75.0%; Pred. No. 5.5e+03; Matches 15; Conservative 0; Mismatches 5; Indels
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RESULT 10
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Patent No. 5821062
GENERAL INFORMATION:
APPLICANT: KOMAL, KOICHITO
APPLICANT: KANEKO, Hideo
APPLICANT: NAKATSUKA, IWAO
TITLE OF INVENTION: OLIGONUCLEOTIDE FOR USE IN CHECKING
TITLE OF INVENTION: PRESENCE OR ABSENCE OF MUTATION IN
TITLE OF INVENTION: HUMAN-DERIVED CYTOCHROME P450IIC18 GENE
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP STREET: P.O. Box 747
CITY: Falls Church
STAME: Virginia
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    synthetic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 60.0%; Score 12; DB 3; 1
Best Local Similarity 75.0%; Pred. No. 5.5e+03;
Matches 15; Conservative 0; Mismatches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
COMPUTER: IBM PC
OPERATING SYSTEM: IBM DOS Version 5.00
REGISTRATION NUMBER: 38,347

REFERENCE/DOCKET NUMBER: 07265/146001

TELECOMMULICATION INFORMATION:
TELEPAX: 619/678-5070
TELEPAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 113:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

APPLICATION NUMBER: US/08/716,459
FILING DATE: 27 SEPTEMBER 1996
CLASSIFICATION: 536
(PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP-059385/1994
FILING DATE: 29-03-1994
FILING DATE: 29-03-1994
FILING DATE: 29-03-1994
FILING DATE: 39-03-1994
FILING DATE: 39-03-1994
FILING DATE: 30-03-1094
FILING DATE: 30-03-1094
FILING DATE: 29-03-1094
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GACCGCATAGACTTCTCAGA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GACCCACACCTATTCAGA 20
                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: Genomic DNA US-09-038-637-113
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 8
US-08-716-459-1/C
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GENERAL INFORMATION:
APPLICANT: Lacroix, Jean-Michel
APPLICANT: Lacroix, James M.
ATILLE OF INVENTION: METHOD AND KIT FOR QUANTITATION AND
TITLE OF INVENTION: MUCHEIC ACID SEQUENCING OF NUCLEIC ACID ANALYTES IN A SAMPLE NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
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                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: amplification primer CT1431F for cryptic; OTHER INFORMATION: plasmid US-08-819-912-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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59.0%; Score 11.8; DB 1; Length 18; 86.7%; Pred. No. 6.9e+03; ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER FRADABLE FORM:
MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb storage COMPUTER: IBM COMPACTIBLE COMPATINE SYSTEM: MS DOS SOFTWARE: Word Perfect CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/819,912
                                                                                                                                                                                                                                                                                                                                                                                       ...urESSE: Oppedahl & Larson
STREET: 1992 Commerce Street Suite 309
CITY: Yorktown
STATE: NY
COUNTRY: US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MYLECULE TYPE: other nucleic acid
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ANTI-SENSE: yes
FRAGMENT TYPE: internal
ORIGIMAL SOURCE:
ORGANISM: Chlamydia trachomatis
                                                                                                                                                                                                                                     Sequence 8, Application US/08819912
Patent No. 5795722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Larson, Marina T.
REGISTRATION NUMBER: 32,038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: VC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (914) 245-3252
TELEFAX: (914) 962-4330
                                                                                        6 CATAGACTTCTCAGA 20
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                                                                                                                  16 CATAGACTTTTGAGA 2
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    Query Match
Best Local Similarity 86.7
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10598
                                                                                                                                                                                                                      US-08-819-912-8
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APPLICANT: Akong, Michael A. APPLICANT: Akong, Michael A. APPLICANT: Akong, Michael M. APPLICANT: Akong, Michael M. APPLICANT: Welicelebi, G. APPLICANT: Burbet, Paul G. APPLICANT: Burbet, Paul G. TITLE OF INVENTION: AUTOMATED ANALYSIS EQUIPMENT AND ASSAY METHOD FOR DETECTING CELL FITTLE OF INVENTION: PROTEIN FUNCTION USING SAME TITLE OF INVENTION: PROTEIN FUNCTION NUMBER: US/08/229,150 CURRENT FILING DATE: 1994-04-18 EARLIER APPLICATION NUMBER: 07/812,254 EARLIER PILING DATE: 1991-12-20 NUMBER OF SEQ ID NOS: 4 SOOFWARE: Patentin Ver. 2.0 SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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Pred. No. 1.1e+04;
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                                       ISBE: Brown, Martin, Haller & McClain
: 1660 Union Street
San Diego
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                             COMPUTER: 148 COMPOTED COURDED COMPOTER: 158 COMPUTER: 158 COMPOTED COURDED CO
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92.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
NYMOTETICAL: NO
                                                                                                                                                                                                                                                                                                            IBM Compatible
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INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                               STATE: CA
COUNTRY: USA
ZIP: 92101-2926
COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 ATAGACTTCTCAG 19
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Best Local Similarity 92.3
Matches 12; Conservative
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                      CORRESPONDENCE ADDRESS: ADDRESSER: Brown, Ma
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                            COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-434-511-4
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METHOD FOR DETECTING CELL SURFACE PROTEIN FUNCTION USING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/291,932A
FILING DATE: AUGUSE 15, 1994
CLASSIFICATION DATA:
FRIOR APPLICATION DATA:
FRIOR APPLICATION DATA:
FRIOR APPLICATION DATA: including application
FRIOR APPLICATION DATA: described below:
APPLICATION NUMBER: 08/245,466
FILING DATE: May 18, 1994
APPLICATION NUMBER: 07/987,132
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
ANAMER MAGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 1.1e+04;
4; Mismatches 1
                   Sequence 289, Application US/08291932A
Patent No. 5658780
GENERAL INFORMATION:
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Braper, Kenneth G.
APPLICANT: McSwiggen, James
TITLE OF INVENTION: RIBOZYME TREATMENT OF
TITLE OF INVENTION: RELATED TO LEVELS OF
TITLE OF INVENTION: RF-KB
TITLE OF INVENTION: RF-KB
TITLE OF INVENTION: RF-KB
TITLE OF INVENTION: RF-KB
NUMBER OF SEQUENCES: 830
CORRESPONDENCE ADDRESS:
ADDRESSER: Lyon & Lyon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REPRENCE/DOCKET WUMBER: 208/157
TELEPHONE: (213) 489-1600
TELEPAX: (213) 955-0440
TELEFAX: (213) 955-0440
INFORMATION FOR SEQ ID NO: 289: SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-434-511-4/c
; Sequence 4, Application US/08434511
; Patent No. 6057114
; GENERAL INFORMATION:
; APPLICANT: Akong, Anthony
; APPLICANT: Velicelebi, Gonul
; APPLICANT: Parbol, Gonul
; TITLE OF INVENTION: METHOD FOR DET
                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57.0%;
61.5%;
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1 AUGGACUUCUCAG 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TOPOLOGY: linear
US-08-291-932A-289
   US-08-291-932A-289
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Sequence 1239, Application US/09696791

Sequence 1239, Application US/09696791

Patent No. 6770633

GENERAL INFORMATION:

APPLICANT: Robbins, Joan M.

APPLICANT: Tritz, Richard

TITLE OF INVENTION: RIBOZYME THERAPY FOR THE TREATMENT OF PROLIFERATIVE

TITLE OF INVENTION: SIT AND EYE DISEASES

TITLE OF INVENTION: SIT AND EYE DISEASES

FILE REFERENCE: 480144.407

CURRENT RILING DATE: 2000-10-25

NUMBER OF SEQ ID NOS: 4523

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 1239
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Batent No. 6025194

GENERAL INFORMATION:
APPLICANT: Funk, Walter
TITLE OF INVENTION: Methods for Modulating and Identifying
TITLE OF INVENTION: Cellular Senescence
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Geron Corporation
STREET: 230 Constitution Drive
                                                                                                                                                                                                                                                                     Score 11.4; DB 4; Length 19;
Pred. No. 1.1e+04;
0; Mismatches 1; Indels
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                                                                                                                                                                                                               ; OTHER INFORMATION: Cdk-we-hu ribozyme binding site US-09-696-791-1238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 11.4; DB 4;
Pred. No. 1.1e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
TITLE OF INVENTION: SKIN AND EYE DISEASES FILE REFERENCE: 480124.407 CURRENT PAPPLICATION NUMBER: US/09/696,791 CURRENT FILING DATE: 2000-10-25 NUMBER OF SEQ ID NOS: 4523 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 1238 LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                         57.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 92.3%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 GCATAGACTICTC 17
                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 92.3
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                    S GCATAGACTICTC 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                            TYPE: DNA ORGANISM: Homo sapiens
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: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-696-791-1239/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
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                       TYPE: DNA

CRGANISM: Artificial Sequence

COTHER INFORMATION: Description of Artificial Sequence:

CTHER INFORMATION: Oligonucleotide used for screening of products having

CTHER INFORMATION: EcoRI site adjacent to initiation codon of human

US-08-229-150-4

US-08-229-150-4
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Patent No. 6770633
GENERAL INFORMATION:
APPLICANT: Robbins, Joan M.
APPLICANT: Tritz, Richard
TITLE OF INVENTION: RIBOZYME THERAPY FOR THE TREATMENT OF PROLIFERATIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                   Length 17;
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Pred. No. 1.1e+04;
                                                                                                                                                                                                                                                                                                                                                                    RESULT 13
5401629-5/c
; Patent No. 5401629
; TITLE OF INVENTION ASSAY METHODS AND COMPOSITIONS USFUL
; FOR MEASURING THE TRANSDUCTION OF AN INTRACELLULAR SIGNAL
; NUMBER OF SEQUENCES: 5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/563,751
; FILING DATE: 07-AUG-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 14
5401629-5/c
i. Patent No. 5401629
i. Patent No. 5401629
i. TILLE OF INVENTION: ASSAY METHODS AND COMPOSITIONS USEFUL
i. FOR MEASURING THE TRANSDUCTION OF AN INTRACELLULAR SIGNAL
i. WUMBER OF SEQUENCES: 5
CURRENT APPLICATION DATA:
i. APPLICATION NUMBER: US/07/563,751
i. FILING DATE: 07-AUG-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                 Score 11.4; DB 3;
Pred. No. 1.1e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 11.4; DB 6;
Pred. No. 1.1e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     57.0%;
92.3%;
                                                                                                                                                                                                 57.0%;
92.3%;
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92.3%;
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Best Local Similarity 92.3
                                                                                                                                                                                                                                                                               7 ATAGACTICTCAG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 92.3
Best Local 12; Conservative
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                                                                                                                                                                                                                     Best Local Similarity 92.3
Matches 12; Conservative
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US-09-696-791-1238/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO:5:
LENGTH: 17
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           LENGTH: 17
                                                                                                                                                                                                   Query Match
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Gaps

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GENERAL INFORMATION:

APPLICANT: Bai. Chang
APPLICANT: Bai. Chang
APPLICANT: Liu, Xiaomei
TITLE OF INVENTION:
TITLE OF INVENTION: DNA MOLECULES ENCODING HUMAN NHL, A DNA
TITLE OF INVENTION: DNA MOLECULES ENCODING HUMAN NHL, A DNA
TITLE OF INVENTION: DATE: 20585P
CURRENT APPLICATION NUMBER: US/10/148,806
CURRENT FILING DATE: 2002-06-05
PRIOR APPLICATION NUMBER: 05/605
PRIOR APPLICATION NUMBER: 60/169,970
PRIOR PILING DATE: 1999-12-09
PRIOR FILING DATE: 1999-12-09
PRIOR FILING DATE: 1999-12-09
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 21
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match 57.0%; Score 11.4; DB 4; Best Local Similarity 92.3%; Pred. No. 1.1e+04; Matches 12; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: oligonucleotide
US-10-148-806-21
Sequence 21, Application US/10148806
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                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8 TAGACTTCTCAGA 20
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ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 20
US-09-422-978-4697
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Bai, Chang
APPLICANT: Metsger, Michael
APPLICANT: Metsger, Michael
APPLICANT: Metsger, Michael
APPLICANT: Michael
APPLICANT: Metsger, Michael
APPLICANT: Michael
APPLICANT: Michael
APPLICANT: Michael
APPLICANT: Michael
APPLICANT: Michael
TITLE OF INVENTION: HELICASE
FILE REFERENCE: 20585P
CURRENT APPLICATION NUMBER: US/10/148,806
CURRENT FILING DATE: 2002-06-05
PRIOR FILING DATE: 2000-12-09
PRIOR FILING DATE: 1999-12-09
NUMBER OF SEQ ID NOS: 38
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57.0%; Score 11.4; DB 4; Length 20; 92.3%; Pred. No. 1.1e+04; Live 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 11.4; DB 3; Length 20;
Pred. No. 1.1e+04;
0; Mismatches 1; Indels
              OPERATION SYSTEM:
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,180
FILING DATE: 19-NOV-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kaster, Kevin R.
REGISTRICATION NUMBER: 206
TELECOMMUNICATION NUMBER: 206
TELECOMMUNICATION NUMBER: 206
TELECOMMUNICATION INFORMATION:
TELEFAX: (650) 473-8654
INPORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLLOGY: linear
MOLECTUE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | NAME/KEY: - | LOCATION: 1..20 | COCATION: 1..20 | CTHEN INFORMATION: /note= "primer 92-5'" US-08-974-180-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: oligonucleotide US-10-148-806-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 20, Application US/10148806
Patent No. 6762042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             57.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S GCATAGACTTCTC 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8 TAGACTICICAGA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12; Conservative
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Matches 12; Conservative
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Best Local Similarity
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Gaps

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Length 20; Indels

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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Cohen. Daniel
APPLICANT: Chem. Daniel
APPLICANT: Blumenfeld, Marta
APPLICANT: Blumenfeld, Marta
APPLICANT: Chumakov, Ilya
APPLICANT: Chumakov, Ilya
TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
FILE REFERENCE: GENSET.020CP1
CURRENT APPLICATION NUMBER: US/09/422, 978
CURRENT APPLICATION NUMBER: US 09/298,850
EARLIER PILING DATE: 1999-10-20
EARLIER PILING DATE: 1999-10-20
EARLIER PILING DATE: 1998-11-23
EARLIER PILING DATE: 1998-11-23
EARLIER FILING DATE: 1998-04-21
NUMBER OF SEQ ID NOS: 11796
SEQ ID NO 4697
LENGTH: 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; LOCATION: 1..18 ......; OTHER INFORMATION: upstream amplification primer 99-17105 for SEQ 763, US-09-422-978-4697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match

56.0%; Score 11.2; DB 4; Length 18;
Best Local Similarity 81.2%; Pred. No. 1.46+04;
Matches 13; Conservative 0; Mismatches 3; Indels
Sequence 4697, Application US/09422978 Patent No. 6537751
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RESULT 21

RESULT 19 US-10-148-806-21

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US-09-249-730-204/C

Sequence 204, Application US/09249730

Sequence 204. Application US/09249730

Sequence 204. Application US/09249730

GENERAL INFORMATION:

APPLICANT: WRIGHT, Jim A.

TITLE OF INVENTION: Antitumor Antisense Sequences Directed Against R1 and TITLE OF INVENTION: R2 Components of Ribonucleotide Reductase

FILLE REPRENCE: 032306-040;

FILLE REPRENCE: 032306-040;

CURRENT APPLICATION NUMBER: US/09/249,730

CURRENT FILING DATE: 1999-02-11
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ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5948611ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 20;
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                                                                                                                                                                                                                                                   COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 3.1
SOFTWARE: WORDERFECT 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256,426B
FILING DATE: 03-FEB-1995
CLASSIFICATION NUMBER: PCT/US93/10964
FILING DATE: 12-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,284
FILING DATE: 13-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Mark Defluca
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TUT-1082
TELECOMMUTCATION INFORMATION:
                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 113
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 ACCGCATAGACTTCTC 17
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 204
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: NUCLEIC ACID
STRANDEDNESS: SINGI
TOPOLOGY: LINEAR
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
CRGANISM: Human
US-09-249-730-204
                                                                                                                                                                   19103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-256-426B-113
                                                                                                    STATE: P. COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGIH:
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                                                                                      APPLICANT: Prockop, Darwin J.
APPLICANT: Ala-Kokko, Leena
APPLICANT: Ala-Kokko, Leena
APPLICANT: Ala-Kokko, Leena
APPLICANT: Ritvaniemi, Pertti
APPLICANT: Ritvaniemi, Pertti
APPLICANT: Balawin, Clinton
APPLICANT: Hopkinson, Ian
APPLICANT: Ahmad, Nilofer Nina
TITLE OF INVENTION: PREDISPOSITION FOR OSTEOARTHRITIS
NUMBER OF SEQUENCES: 261
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 5558988ris
STREET: One Liberty Place, 46th floor
STREET: Date of the control of the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Pred. No. 1.5e+04;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Hopkinson, Ian
APPLICANT: Ahmad, Nilofer Nina
ITLE OF INVENTION: Methods of Detecting A Genetic
NUMBER OF SEQUENCES: 293
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WordPerfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/977,284A

FILING DATE: 13-NOV-1992

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

RILING DATE:

FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY AGENT INFORMATION:
NAME: DeLuca, Mark
REGISTATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-0697
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEPHONE: (215) 568-3139
INFORMATION FOR SEQ ID NO: 113:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 113, Application US/08256426B
; Patent No. 5948611
; GENERAL INFORMATION:
                                 Sequence 113, Application US/07977284A
Patent No. 5589808
GENERAL INSTRANTION:
APPLICANT: Prockop, Darwin J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Prockop, Darwin J.
Ala-Kokko, Leena
Williams, Charlene J.
Ritvaniemi, Pertri
Baldwin, Clinton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     56.0%;
81.2%;
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Best Local Similarity 81.2
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TOPOLOGY: LINEAR; ANTI-SENSE: NO US-07-284A-113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
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          US-07-977-284A-113
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COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
APPLICANT:
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APPLICANT:
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APPLICANT:
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Sequence 28, Application US/09975123
Patent No. 6750019
GENERAL INFORMATION:
APPLICANT: Susan M. Freier
TITLE OF INVENTION: ANTISENSE MODULATION OF INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN
TITLE OF INVENTION: ARRESSION
FILE REPERENCE: RTS-0253
CURRENT APPLICATION NUMBER: US/09/975,123
CURRENT FILING DATE: 2001-10-09
NUMBER OF SEQ ID NOS: 43
SEQ ID NO 28
LENGTH: 20
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Patent No. 6770461

GENERAL INFORMATION:
APPLICANT: Carulli, John P.
APPLICANT: Little, Randall D.
APPLICANT: Little, Robert R.
APPLICANT: Lohnson, Mark L.
TILLE OF INVENTION: High bone mass gene of 11q13.3
FILE REFERENCE: 032796-013
CURRENT APPLICATION UNMER: US/09/544,398B
CURRENT PILING DATE: 2002-06-10
PRIOR APPLICATION NUMBER: US 60/011,449
PRIOR FILING DATE: 1998-01-13
SPRIOR FILING DATE: 1998-01-13
SPRIOR FILING DATE: 1998-01-13
SPRIOR FILING DATE: 1998-10-13
SPRIOR FILING DATE: 1908-01-13
SPRIOR FILING DATE: 1908-01-13
SPRIOR FILING DATE: 1908-01-13
SPRIOR FILING DATE: 1908-01-13
SPRIOR FILING DATE: 1908-10-23
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Antisense Oligonucleotide US-09-975-123-28
                      EARLIER FILING DATE: 1996-08-02
EARLIER APPLICATION NUMBER: US 60/039,959
EARLIER FILING DATE: 1997-03-07
EARLIER FILING DATE: 1997-08-01
MUMBER OF SEQ ID NOS: 220
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: 204
LENGTH: 20
EARLIER APPLICATION NUMBER: US 60/023,040
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ORGANISM: Artificial Sequence
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Matches 13; Conserv
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ORGANISM: Human
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US-09-544-398B-32/c
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US-09-975-123-28/c
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US-09-198-452A-3744/C
US-09-198-452A-3744/C
Sequence 3744, Application US/09198452A
Sequence 3744, Application US/09198452A
Sequence 3744, Application US/09198452A
Sequence 3744, Application US/09198452A
GENERAL INFORMATION:
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevering of INVENTION: and treatment of infection
TITLE OF INVENTION: and treatment of infection
TITLE OF INVENTION: 1999
CURRENT APPLICATION NUMBER: US/09/198,452A
CURRENT PILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 6849
SEQ ID NO 3744
LENGTH: 20
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Patent No. 6593305
| GENERAL INFORMATION:
| APPLICANT: WIGHT, Jim A.|
| TITLE OF INVENTION: Antitumor Antisense Sequences Directed Against R1 and |
| TITLE OF INVENTION: Antitumor Antisense Sequences Directed Against R1 and |
| TITLE OF INVENTION: R2 Components of Ribonucleotide Reductase |
| FILE REPERENCE: 032396-023 |
| CURRENT APPLICATION NUMBER: US/09/249,247 |
| CURRENT FILING DATE: 1999-02-11
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                                                                                        Sequence 36, Application US/09359756

Sequence 36, Application US/09359756

GENERAL INFORMATION:

APPLICANT: Brett P. Monia

APPLICANT: William Gaarde

APPLICANT: Lex M. Cowsert

TITLE OF INVENTION: ANTISENSE MODULATION OF MEKKI EXPRESSION

TITLE OF INVENTION: ANTISENSE MODULATION OF MEKKI EXPRESSION

FILE REFERENCE: RTS-0077

CURRENT FILING DATE: 1999-07-23

NUMBER OF SEQ ID NOS: 47

SEQ ID NO 36

LENGTH: 20
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Pred. No. 1.5e+04;
0; Mismatches 3;
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; OTHER INFORMATION: Antisense Oligonucleotide
US-09-359-756-36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 56.0%;
Best Local Similarity 81.2%;
Matches 13; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence
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Best Local Similarity 81.2%;
Matches 13; Conservative
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US-09-249-247-204/c
                                                         RESULT 24
US-09-359-756-36/c
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Gaps

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Sequence 4, Application US/08357791

Sequence 4. Application US/08357791

Patent No. 5652102

GENERAL INFORMATION:
APPLICANT: Fratamico, Pina M.
APPLICANT: Sackitey, Soloman K.
APPLICANT: Wiedmann, Martin
TITLE OF INVENTION: Assay for Enterohemorrhagic Escherichia
TITLE OF INVENTION: coli 0157:H7 by the Polymerase Chain Reaction
NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                 ;
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                                                                                                                                                                                                                                                                                    55.0%; Score 11; DB 4; Length 18; 100.0%; Pred. No. 1.8e+04; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Carull, John P.

APPLICANT: Little, Randall D.

APPLICANT: Recker, Robert R.

APPLICANT: Recker, Robert R.

TITLE OF INVENTION: High bone mass gene of 11q13.3

FILE REFRERENCE: 032796-014

CURRENT APPLICATION NUMBER: US/09/543,771B

CURRENT FILING DATE: 2000-04-05

PRIOR APPLICATION NUMBER: US 60/071,449

PRIOR PRILING DATE: 1998-01-13

PRIOR FILING DATE: 1998-01-13

PRIOR FILING DATE: 1998-01-23

NUMBER OF SEQ ID NOS: 641

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 6:99
                                                                                                                                                                                                          ; OTHER INFORMATION: Artificial sequence is a primer. US-09-543-771B-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PEATURE: OTHER INFORMATION: Artificial Sequence is a primer
PRIOR APPLICATION NUMBER: US 60/105,511
PRIOR FILING DATE: 1998-10-23
NUMBER OF SEQ ID NOS: 641
SEQTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 32
LENGTH: 18
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8.09-543-711B-629/c
; Sequence 629, Application US/09543771B
; Patent No. 6780609
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                      ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                      Query Match 55.0
Best Local Similarity 100.
Matches 11; Conservative
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Matches 11; Conservative
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17 GACTTCTCAGA 7
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US-09-543-771B-629
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US-08-357-791-4
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                                                                                                                                                 TYPE: DNA
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US-09-544-398B-629/C

Sequence 629, Application US/09544398B

Patent No. 6770461

GENERAL INFORMATION:

APPLICANT: Carulli, John P.

APPLICANT: Little, Randall D.

APPLICANT: Little, Randall D.

APPLICANT: Dohnson, Mark L.

ITLE OF INFORMATION: High bone mass gene of 11q13.3

FILE REFERENCE: 032796-013

CURRENT APPLICATION NUMBER: US/09/544,398B

CURRENT FILING DATE: 2002-06-10

PRIOR APPLICATION NUMBER: US 60/071,449

PRIOR APPLICATION NUMBER: US 60/071,449

PRIOR APPLICATION NUMBER: US 60/071,449

PRIOR APPLICATION NUMBER: US 60/105,511

PRIOR APPLICATION NUMBER: US 60/105,511

PRIOR APPLICATION NUMBER: US 60/105,511

SEQ ID NO 628

SEQ ID NO 628

LENGTWARE: FastSEQ for Windows Version 4.0
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US-09-543-771B-32/C

j Sequence 32, Application US/09543771B

pacent No. 6780609

GENERAL INFORMATION:
APPLICANT: Carulli, John P.
APPLICANT: Little, Randall D.
APPLICANT: Little, Randall D.
APPLICANT: Hocker, Robert R.
APPLICANT: Johnson, Mark L.
TITLE OF INVENTION: High bone mass gene of 11q13.3
FILE REFERENCE: 032796-014
CURRENT APPLICATION NUMBER: US/09/543,771B
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 09/229,319
PRIOR FILING DATE: 1999-01-13
PRIOR FILING DATE: 1998-01-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Artificial Sequence is a primer. Patent No. 6770461
US-09-544-398B-629
                                                                                                 FEATURE:
, OTHER INFORMATION: Artificial sequence is a primer
US-09-544-398B-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                55.0%; Score 11; DB 4; Le 100.0%; Pred. No. 1.8e+04; tive 0; Mismatches 0;
                                                      TYPE: DNA ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
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Best Local Similarity 100.
Matches 11; Conservative
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17 GACTTCTCAGA 7
       SEQ ID NO 32
LENGTH: 18
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US-09-659-791A-37/c
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Patent No. 6333152

GENERAL INFORMATION

GENERAL INFORMATION:

APPLICANT: Kinzler, Kenneth

APPLICANT: Zhang, Lin

APPLICANT: Zhang, Lin

APPLICANT: Zhang, Lin

APPLICANT: Zhang, Lin

TITLE OF INVENTION: Gene Expression Profiles in No. 6333152mal and

TITLE OF INVENTION: Cancer Cells

FILE REFERENCE: 01107.74664

CURRENT APPLICATION NUMBER: US/09/081,646

CURRENT FILING DATE: 1998-05-20
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Pred. No. 2.3e+04;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/357,791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55.0%; Score 11; DB 1; Le 100.0%; Pred. No. 1.9e+04; tive 0; Mismatches 0;
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EARLIER FILING DATE: 1997-05-21
NUMBER OF SEQ ID NOS: 871
SEQ ID NO 202
LENGTH: 15
: Bldg. 005, Rm 411, BARC-West
Beltsville
                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                     CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Graeter, Janelle S.
REGISTRATION NUMBER: 35,024
REFERENCE/POCKET NUMBER: D.N.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-504-5676
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : Escherichia coli
0157:H7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-081-646-202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 12; Conserva
                                                               U.S.A.
                                                                                                                                                                                                                                       FILING DATE:
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US-09-081-646-202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; STRAIN:
US-08-357-791-4
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6 CATAGACTTCTCAG 19

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Sequence 5, Application US/09124398A
Patent No. 6770456
GENERAL INFORMATION:
APPLICANT: Coulie, Pierre
APPLICANT: Boon-Falleur Thierry
TITLE OF INVENTION: ENDOGENOUS RETROVIRUS TUMOR ASSOCIATED NUCLEIC ACIDS AND ANTIGENS
FILE REFERENCE: LO461/7033
CURRENT APPLICATION NUMBER: US/09/124,398A
CURRENT PILING DATE: 1998-07-29
NUMBER OF SEQ ID NOS: 43
SOFTWARE FastSEQ for Window Version 3.0
SEQ ID NO 5
LENGTH: 18
                                                                                                                                                          APPLICANT: Kenneth
APPLICANT: Conservations
APPLICANT: Conservation
APPLICANT Conservation
APPLICANT
APPLI
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APPLICANT: Susan M. Freier
TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 10.8; DB 4; Length 18; Pred. No. 2.3e+04; 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 10.8; DB 3; Length 15; Pred. No. 2.3e+04;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
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US-09-081-646-743
; Sequence 743, Application US/09081646
; Patent No. 6333152
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54.0%;
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Best Local Similarity 85.77
Matches 12; Conservative
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Best Local Similarity 85.7
Matches 12; Conservative
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CORGANISM: Homo sapiens
US-09-124-398-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-081-646-743
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Indels
                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Pavecy, Pamela
APPLICANT: Pavecy, Pamela
APPLICANT: McSwiggen, James
APPLICANT: Stinchcomb, Dan T.
APPLICANT: CONDITIONS RELATED TO LEVELS
TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
TITLE OF INVENTION: GROWTH PACTOR
NUMBER OF SEQUENCES: 8502
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
4 ;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOCTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/584,040
FILING DATE: January 11, 1996
CLASSIFICATION DATA:
APPLICATION NUMBER: 60/005,974
FILING DATE: OCTOBER 26, 1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 39
US-09-371-772B-2242/c
US-09-371-772B-2242, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
                                                                                                                                                                          US-08-584-040-5340/c
; Sequence 5340, Application US/08584040
; Patent No. 6346398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               218/064
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INFORMATION FOR SEQ ID NO: 5340:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Warburg, Richard J. REGISTRATION NUMBER: 32,327 REFERENCE/DOCKET NUMBER: 216 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 CCGCATAGACTICTCAG 19
                                           1 GACCGCATAGACTTCTC 17
                                                                                   1 GACAGCAUAGACGACAC 17
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(213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17 CCGCAAAGAAGTCACAG
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Matches 13; Conservative
12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-584-040-5340
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  Matches
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Pred. No. 3e+04;
                                                                                                                                                                                                                                                                     Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gequence 399, Application US/08985162
Facent No. 6057156
GENERAL INFORMATION:
APPLICANT: Achtar, Saghir
APPLICANT: Pall, Patricia
APPLICANT: McSwiggen, James
TITLE OF INVENTION: ENZIMATE
TITLE OF INVENTION: TO LEVELS OF EPIDERMAL
TITLE OF INVENTION: PACTOR RECEPTORS
TITLE OF INVENTION: PACTOR RECEPTORS
TITLE OF SEQUENCES: 1877
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                2; Indels
                                                                                                                                                                                                                                                                  Score 10.8; DB 3;
Pred. No. 2.4e+04;
                                                                                                                                                                          FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-659-791A-37
                                                                                                                                                                                                                                                                                                                Mismatches
FILE REFERENCE: RTS-0156
CURRENT APPLICATION NUMBER: US/09/659,791A
CURRENT FILING DATE: 2000-09-11
NUMBER OF SEQ ID NOS: 90
SEQ ID NO 37
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastESEQ for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,162
FILING DATE: 04 December 1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION TOWNER: 06/036,476
FILING DATE: 31 January 1997
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
RECISTRATION NUMBER: 230,107
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Lyon & Lyon
STREET: 613 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                  Query Match

Best Local Similarity 85.7%; Pr
Matches 12; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 399:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             53.0%;
70.6%;
                                                                                                                               TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                            2 ACCGCATAGACTTC 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGIH: 17 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: U.S.A. ZIP: 90071-2066
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US-08-985-162-399
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Gaps

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Query Match 53.0%; Score 10.6; DB 4; Length 17; Best Local Similarity 70.6%; Pred. No. 3e+04; Matches 12; Conservative 1; Mismatches 4; Indels
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Job time : 98 secs
                                                                                                                                                                                                                                                                                                                                                    1 GACCGCATAGACTTCTC 17
                                                                                                                                                                                                                                                                                                                                                                               (213) 955-0440
             TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 3 SEQUENCE CHARACTERISTICS: LENGTH: 17 base pairs TYPE: mucleic acid STRANDEDNESS: single
                                                                                                                                                                       linear
                                                                                                                                                                       ;
TOPOLOGY:
US-09-401-063-399
                                                              AFFLICANT: StinchComb, Dam
APPLICANT: StinchComb, Dame
APPLICANT: Escobedo, Jaime
APPLICANT: Escobedo, Jaime
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
FILE REPERENCE: MBHB00,876-J (237/198)
CURRENT APPLICATION NUMBER: US (90/0371,772B
CURRENT PILING DATE: 1999-08-10
PRIOR FILING DATE: 1995-01-08
PRIOR FILING DATE: 1996-01-08
NUMBER OF SEQ ID NOS: 14225
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Akhlar, Saghir
APPLICANT: Akhlar, Saghir
APPLICANT: Akhlar, Saghir
APPLICANT: McSwiggen, James
TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT
TITLE OF INVENTION: OF DISEASES OR CONDITIONS RELATED
TITLE OF INVENTION: TO LEVELS OF EPIDERMAL GROWTH
TITLE OF INVENTION: PACTOR RECEPTORS
TITLE OF SEQUENCES: 1877
CORRESPONDENCE ANDRESS:
ADDRESSEE: Lyon & Lyon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastERQ for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/401,063
  APPLICANT: Ribozyme Pharmaceuticals, Inc. APPLICANT: Pavco, Pam
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/985,162
FILLING DATE: 04 December: 1997
APPLICATION NUMBER: 60/036,476
FILLING DATE: 31 January 1997
ATTORNEY, AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 399, Application US/09401063; Patent No. 6623962; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 230
TELECOMMUNICATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 CCGCATAGACTTCTCAG 19
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                                                    McSwiggen, Jim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: RNA
CRGANISM: Mus sp.
US-09-371-772B-2242
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US-09-401-063-399
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GenCore version (c) 1993 - 2005

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nucleic search, using sw model

OM nucleic -

on: Run Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 20

Post-processing:

Minimum Match 0% Maximum Match 100% Listing first 100 summaries

Published_Applications_NA:*

Database

7305758 segs, 3244068913 residues

Gapop 10.0 , Gapext 1.0

IDENTITY NUC

Scoring table:

Searched:

Perfect score:

Sequence:

gaccgcatagacttctcaga 20

US-09-743-825-10

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Sequence 31, Appl
Sequence 46, Appl
Sequence 14, Appl
Sequence 289, Appl
Sequence 289, Appl
Sequence 43, Appl
Sequence 43, Appl
Sequence 20, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 22, Appl
Sequence 24, Appl
Sequence 2082, Appl
Sequence 2083, Appl
Sequence 2084, Appl
Sequence 73759, A Sequence 196, App Sequence 119, App Sequence 11, Appl Sequence 113, App Sequence 137, App Sequence 337, App Sequence 337
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1 US-10-741-600-73759

1 US-10-136-136-136

1 US-10-136-136-139

1 US-10-956-250-11

1 US-10-956-250-11

1 US-10-923-329-137

2 US-10-923-329-99

2 US-10-148-806-21

2 US-10-148-806-21

2 US-10-148-806-21

2 US-10-148-806-21

2 US-10-144-99-99

2 US-10-148-806-21

2 US-10-148-806-21

2 US-10-148-806-21

2 US-10-131-901A-2089

2 US-10-131-901A-2089

3 US-10-131-901A-2089

4 US-10-157-318-99

5 US-10-157-318-99

6 US-10-157-318-99

6 US-10-157-106-99

6 US-10-157-106-99

6 US-10-157-106-99

6 US-10-157-118-99

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| (cgn2 6/ptodata/2/pubpna/US06_NEW PUB.seq:*
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| (cgn2 6/ptodata/2/pubpna/US06_NEW PUB.seq:*
| (cgn2 6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
| (cgn2 6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
| (cgn2 6/ptodata/2/pubpna/US10_NEW PUB.seq:*
| (cgn2 6/ptodata/2/pubpna/US10_NEW PUB.s
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Sequence 2812, Ap	Sequence 48, Appl	Sequence 12, Appl	Sequence 499, App	Sequence 2106, Ap	Sequence 75, Appl	Seguence 187, App
SUMMARIES	ΩΙ	17 US-10-289-762-2812	US-10-007-010-48	US-10-956-250-12	US-09-864-785-499	US-09-864-785-2106	US-10-702-817-75	US-10-365-742-187
	8	17	15	21	σ,	6	22	17
	* Query Match Length DB ID	20	20	20	17	17	18	19
	A Query Match	0.69	0.99	63.0	62.0	62.0	61.0	61.0
	Score	13.8	13.2	12.6	12.4	12.4	12.2	12.2
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Description	Sequence 2812, Ap	Sequence 48, Appl	Sequence 12, Appl	Sequence 499, App	Sequence 2106, Ap	Sequence 75, Appl	Sequence 187, App
ength DB ID	20 17 US-10-289-762-2812	US-10-007-010-48	US-10-956-250-12	US-09-864-785-499	US-09-864-785-2106	US-10-702-817-75	US-10-365-742-187
DB	17	15	21	0	6	22	17
% Query Match Length DB ID	20	20	20	17	17	18	19
Query Match	69.0	0.99	63.0	62.0	62.0	61.0	61.0
Score	13.8	13.2	12.6	12.4	12.4	12.2	12.2
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                                    Gaps
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Length 20,
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                                    Indels
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COMBUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FASTESEQ for Windows
SOFTWARE: FASTESEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/956,250
FILING DATE: 01-0ct-2004
CLASSIFICATION OF STANDARD TO CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/920,559
FILING DATE: 27-Aug-1997
APPLICATION NUMBER: US 08/652,265
FILING DATE: 33-MAY-1996
APPLICATION NUMBER: US 08/834,497
FILING DATE: 13-UNJ-1997
APPLICATION NUMBER: US 08/834,497
FILING DATE: 13-UNJ-1997
APPLICATION NUMBER: US 08/866,211
FILING DATE: 13-UNJ-1997
APPLICATION NUMBER: US 08/866,211
FILING DATE: 13-UNJ-1997
APPLICATION NUMBER: US 08/866,211
FILING DATE: 13-UNJ-1997
APPLICATION NUMBER: 28,462
REGISTRATION NUMBER: 28,462
REGISTRATION NUMBER: 28,462
REGISTRATION NUMBER: 28,462
Score 13.2; DB 15;
Pred. No. 5.1e+03;
0; Mismatches 3;
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Pred. No. 1.1e+04;
0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSER: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
                                                                                                                                                                    US-10-956-250-12; Sequence 12, Application US/10956250 Publication No. US20050090430A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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LENGTH: 20 base pairs
                                                                    2 ACCGCATAGACTTCTCAG 19
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STRANDEDNESS: single
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   66.0%;
83.3%;
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Best Local Similarity 78.9%;
Matches 15; Conservative (
                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 13
 Query Match
Best Local Similarity 83.3
Matches 15; Conservative
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US-10-289-762-2812
Sequence 2812, Application US/10289762
Sequence 2812, Application US/10289762
Sequence 2812, Application No. US20040006218A1
GENERAL INFORMATION:
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prever TITLE OF INVENTION: and treatment of infection
FILE REFERENCE: 9710-003-999
CURRENT APPLICATION NUMBER: US/10/289,762
CURRENT FILING DATE: 2003-03-27
NUMBER OF SEQ ID NOS: 6849
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US-10-007-010-48/c

i Sequence 48, Application US/10007010
i Publication No. US20030125275A1
i GENERAL INFORMATION:
APPLICANT: Alexander H. Borchers
APPLICANT: Alexander H. Dobie
ITILE OF INVENTION: ANTISENSE MODULATION OF HCK EXPRESSION
FILE REFREENCE: RTS-0345
CURRENT APPLICATION NUMBER: US/10/007,010
CURRENT FILING DATE: 2001-12-04
NUMBER OF SEQ ID NOS: 87
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69.0%; Score 13.8; DB 17; Length 20; 88.2%; Pred. No. 2.4e+03; ive 0; Mismatches 2; Indels
 US-10-968-432-44
US-10-516-505-108
US-10-314-979-32
US-10-182-936A-32
US-10-731-739-32
US-10-731-739-32
US-10-731-739-32
US-10-477-238A-629
US-10-680-287A-629
US-10-477-173-32
US-10-477-173-85
US-10-477-173-85
US-10-477-173-85
US-10-477-173-85
US-10-484-377-629
US-10-884-377-629
US-10-884-377-629
US-10-884-377-629
US-10-884-377-629
US-10-888-706-1211
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US-10-289-762-2812
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ORGANISM: Artificial Sequence
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Best Local Similarity 88.2°
Matches 15; Conservative
     SEQ ID NO 2812
LENGTH: 20
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Michele et al.
GENETIC POLYMORPHISMS ASSOCIATED WITH
MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
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APPLICANT: Alfano, James R.
APPLICANT: Alfano, James R.
APPLICANT: Cartinhour, Samuel W.
APPLICANT: Cartinhour, Samuel W.
APPLICANT: Tang, Xiaoyan
TITLE OF INVENTION: PSEUDOMONAS AVR AND HOP PROTEINS, THEIR ENCODING
TITLE OF INVENTION: NUCLEIC ACIDS, AND USE THEREOF
FILE REFERENCE: 19603/4112
CURRENT APPLICATION NUMBER: US/10/365,742
CURRENT APPLICATION NUMBER: 60/326,408
PRIOR PLILING DATE: 2002-02-12
PRIOR FILING DATE: 2002-02-12
PRIOR FILING DATE: 2002-05-10
PRIOR FILING DATE: 2002-05-10
SPRIOR FILING DATE: 2002-05-10
SOFTWARE: PATENTIN UNDER: 00/380,185
SEQ ID NO 187
TENNORM: 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 61.0%; Score 12.2; DB 22; Best Local Similarity 82.4%; Pred. No. 1.8e+04; Matches 14; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                             , OTHER INFORMATION: Antisense Oligonucleotide US-10-702-817-75
       CURRENT FILING DATE: 3033-11-06
PRIOR APPLICATION NUMBER: US 09/106,038
PRIOR FILING DATE: 1998-06-26
PRIOR FILING DATE: 1998-06-17
PRIOR PILING DATE: 1999-06-17
PRIOR APPLICATION NUMBER: 09/695,451
PRIOR PILING DATE: 2000-10-24
NUMBER OF SEQ ID NOS: 247
SEQ ID NO 75
LENGTH: 18
CURRENT APPLICATION NUMBER: US/10/702,817
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; Sequence 73759, Application US/10741600
; Publication No. US20050026169A1
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Publication No. US20030204868A1
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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TITLE OF INVENTION:
TITLE OF INVENTION:
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Sequence 2106, Application US/09864785

Sequence 2106, Application US/09864785

Sequence 2106, Application US/09864781

Sequence 2106, Application US/09864781

GENERAL INFORMATION:
APPLICANT: Stinchcomb, Dan
APPLICANT: Draper, Ken
APPLICANT: Draper, Ken
APPLICANT: Bashinghow, Jim
TITLE OF INVENTION: Eavels of NF-Kappa B
TITLE OF INVENTION: Levels of NF-Kappa B
SOFTWARE 2001-05-23
NUMBER OF SEQ ID NOS: 3929
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2106
LENGTH: 17
               Sequence 499, Application US/09864785

Patent No. US20020177568A1

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Stinchcomb, Dan

APPLICANT: Stinchcomb, Dan

APPLICANT: McSwiggen, Jim

TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate

TITLE OF INVENTION: Levels of NP-Kappa B

FILE REPERENCE: 400/022 (MBHB00-812-D)

CURRENT APPLICATION NUMBER: US/09/864,785

CURRENT PLING DATE: 2001-05-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Description of Artificial Sequence: Nycleic Acid
US-09-864-785-499
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Pred. No. 1.4e+04;
4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62.0%; Score 12.4; DB 9; Length 17; 64.3%; Pred. No. 1.4e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Hong Zhang
TITLE OF INVENTION: ANTISENSE MODULATION OF TNFR1 EXPRESSION
FILE REFERENCE: ISPH-0797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 75, Application US/10702817; Publication No. US20040147471A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 64.3%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 3929
SOFTWARE: PatentIn version 3.0
SEQ ID NO 499
                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: RNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: RNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 CATAGACTTCTCAG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ||: |||::|:|||
CAUGGACUUCUCAG 17
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2 CAUGGACUUCUCAG 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 64.3
Matches 9, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 6
US-10-702-817-75/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 5
US-09-864-785-2106
                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
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ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
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TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERICS:
LENGTH: 20 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
                         4 CGCATAGACTTCTCAGA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GACCGCATAGACTICTC 17
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                                                                  3 cacacacacrccrcaga 19
                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: New York
STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-956-250-11
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Sequence 196, Application US/10190366

Publication No. US20040006031A1

GENERAL INFORMATION:
APPLICANT: Susan M. Freier
APPLICANT: Susan M. Freier
APPLICANT: Renneth W. Dobie
TITLE OF INVENTION: ANTISENSE MODULATION OF HMG-COA REDUCTASE EXPRESSION
FILE REPREBRUE: PTS-002
CURRENT APPLICATION NUMBER: US/10/190,366
CURRENT PILING DATE: 2002-07-02
NUMBER OF SEQ ID NOS: 409
SEQ ID NO 196
LENGTH: 20
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Publication No. US20040006031A1
GENERAL INFORMATION:
APPLICANT: Nicholas M. Dean
APPLICANT: Susan M. Freier
APPLICANT: Susan M. Freier
TITLE OF INVENTION: ANTIERNSE MODULATION OF HMG-COA REDUCTASE EXPRESSION
FILE REFERENCE: PTS-0023
CURRENT APPLICANTION UNDER: US/10/190,366
CURRENT PELING DATE: 2002-07-02
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61.0%; Score 12.2; DB 17; Length 20; 82.4%; Pred. No. 1.8e+04; ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                               Length 19;
                                                                                                                                                                                                                                                                                          IndelB
                                                                                                                                                                                                                                            Query Match 61.0%; Score 12.2; DB 21;
Best Local Similarity 82.4%; Pred. No. 1.8e+04;
Matches 14; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Antisense Oligonucleotide
FILE REFERENCE: CL001499
CURRENT PEPLICATION NUMBER: US/10/741,600
CURRENT FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 73997
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 73759
LENGTH: 19
                                                                                                                                                                                                                                                                                                                                   1 GACCGCATAGACTTCTC 17
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                                                                                                                                                                                                                                                                                                                                                                            1 GACAGCACAGACTTCAC 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence
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Best Local Similarity 82.4
Matches 14; Conservative
                                                                                                                                                        TYPE: DNA
CORGANISM: Homo sapiens
US-10-741-600-73759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: M. musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-190-366-389
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US-10-190-366-389
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TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
DIAGNOSIS AND TREATMENT OF IRON MISREGULATION D
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: Windows
OPERATING SYSTEM: Windows
SOFTWARE: FastSEQ for Windows
SOFTWARE: FastSEQ for Windows
CURRENT APPLICATION DATA:
FILING DATE: 01-0ct-2004
CLASSIFICATION: Unknown>
PRIOR APPLICATION: UNMBER: US/08/920,559
FILING DATE: 27-Aug-1997
APPLICATION NUMBER: US 08/652,265
FILING DATE: 23-RAY-1996
FILING DATE: 23-RAY-1996
FILING DATE: 04-ARR-1997
APPLICATION NUMBER: US 08/834,497
FILING DATE: 13-TON-1997
ATTORNEY/AGRIT INFORMATION:
ATTORNEY/AGRIT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 61.0%; Score 12.2; DB 21;
Best Local Similarity 82.4%; Pred. No. 1.8e+04;
Matches 14; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Poissant, Brian M
REGIGTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-0062-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQ ID NO: 11:
RESULT 1.
US-10-956-20-11
US-10-956-250-11
Sequence 11, Application US/10956250
Publication No. US20050090430A1
GENERAL INFORMATION:
APPLICANT: Feder, John N.
Schatzman, Randall C.
Schatzman, Randall C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-863-806-113
; Sequence 113, Application US/09863806
; Publication No. US20020197608A1
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TYPE: nucleic acid
STRANDEDNESS: single
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ORGANISM: Artificial Sequence
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 15; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-923-329-137/c
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                TITLE OF INVENTION: David

TITLE OF INVENTION: DETECTION OF NEOPLASIM BY ANALYSIS OF SALIVA
NUMBER OF SEQUENCES: 195
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FRAESEQ for Windows Version 2.0b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 113, Application US/10754478
Publication No. US20050009040A1
GENERAL INFORMATION:
APPLICANT: Sidransky, David
TITLE OF INVENTION: DETECTION OF NEOPLASIM BY ANALYSIS OF SALIVA
NUMBER OF SEQUENCES: 195
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60.0%; Score 12; DB 9; Length 20; 75.0%; Pred. No. 2.38+04; ive 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM Compatible OPERATING SYSTEM: Windows 95 SOFTWARE: FastSEQ for Windows Version 2.0b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 07265/146001
                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/863,806
FILING DATE: 22-May-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/038,637
FILING DATE: -UNKNOWN>
APPLICATION NUMBER: 08/152,313
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Liea A.
REGISTRATION NUMBER: 38,347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/10/754,478 FILING DATE: 09-Jan-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: Genomic DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 113:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION TELEPHONE: 619/678-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GACCCCACAGCCTATTCAGA 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 619/678-5099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 113:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 92037
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match
Best Local Similarity 75.07
Page 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
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US-10-754-478-113
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GENERAL INFORMATION NO. US20050164968A1
GENERAL INFORMATION:
APPLICANT: Sitna Therapeutics, Inc.
APPLICANT: Sitna Therapeutics, Inc.
APPLICANT: Sitna Therapeutics, Inc.
APPLICANT: Richards, Ivan
APPLICANT: McSwiggen, James
TITLE OF INVENTION: Using Short Interfering Nucleic Acid (siNA)
FILE REPERENCE: 400-525 (MSH846-672)
CURRENT APPLICATION NUMBER: US/10/923,329
CURRENT TILING DATE: 2004-08-20
PRIOR FILING DATE: 2004-08-20
PRIOR FILING DATE: 2004-04-16
PRIOR FILING DATE: 2004-04-16
PRIOR PLICATION NUMBER: US 10/780,447
PRIOR PLICATION NUMBER: US 60/292,217
PRIOR PLICATION NUMBER: US 60/362,016
PRIOR PLILING DATE: 2001-05-18
PRIOR PLILING DATE: 2001-05-18
PRIOR PLILING DATE: 2001-05-18
PRIOR PLILING DATE: 2001-05-18
PRIOR PLILING DATE: 2001-07-20
PRIOR PLILING DATE: 2001-08-13
PRIOR PLILING DATE: 2001-07-20
PRIOR PLILING DATE: 2001-08-13
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NUMBER OF SEQ ID NOS: 514
SOFTWARE: PatentIn version 3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 20;
FILING DATE: 10-MAR-1998
APPLICATION NUMBER: 08/579,233
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: 08/579,233
FILING DATE: 28-DEC-1995
ATTORNEY/AGENT INPORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REGISTRATION NUMBER: 38,347
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELEPAN: 619/678-5070
INFORMATION FOR SEG ID NO: 113:
SEQUENCE CHARACTERISTICS:
ALBNOTH: 20 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 12; DB 21;
Pred. No. 2.3e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ch 60.0%; Score 12; DB 1. Similarity 75.0%; Pred. No. 2.3e 15; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear: TOPOLOGY: linear: MOLECULE TYPE: Genomic DNA SEQUENCE DESCRIPTION: SEQ ID NO: 113: US-10-754-478-113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 137, Application US/10923329
Publication No. US20050164968A1
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TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
                 FILE REFERENCE: CLOOL199
CURRENT APPLICATION NUMBER: US/10/741,600
CURRENT FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 73997
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 73758
LENGTH: 18
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                                                                                                                                                                                                                                                                                                                                                                                             Query Match 58.0
Best Local Similarity 77.8
Matches 14; Conservative
                                                                                                                                                                                                                                                               ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-600-73758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 17
US-09-768-436-31/c
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US-10-923-333
US-10-923-329-333
US-10-923-329-333
US-10-923-329-333
US-10-923-329-333
US-10-923-329-333
US-10-923-329-333
US-10-923-329-333
US-10-923-329-329
Publicartion No. US20050164968A1
APPLICANT: Richards, Ivan
APPLICANT: Richards, Ivan
APPLICANT: Weskiggen, James
TITLE OF INVENTION: NA Interference Mediated Inhibition of ADAM33 Gene Expression
TITLE OF INVENTION: Using Short Interfering Nucleic Acid (sink)
FILE REPERENCE: 400/225 (MEHB04-672)
CURRENT FILING DATE: 2004-08-20
PRIOR APPLICATION NUMBER: PCT/US04/16390
PRIOR APPLICATION NUMBER: US 10/826,966
PRIOR APPLICATION NUMBER: US 10/826,966
PRIOR APPLICATION NUMBER: US 60/292,217
PRIOR APPLICATION NUMBER: US 60/292,217
PRIOR APPLICATION NUMBER: US 60/292,217
PRIOR APPLICATION NUMBER: US 60/392,217
PRIOR PLING DATE: 2001-05-18
PRIOR PLING DATE: 2001-03-18
                                  ; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense US-10-923-329-137
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NUMBER OF SEQ ID NOS: 514
SOFTWARE: Patentin version 3.3
SEQ ID NO 333
LENGTH: 19
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59.0%; Score 11.8; DB 22; Length 19;
Best Local Similarity 66.7%; Pred. No. 2.9e+04;
Matches 10; Conservative 3; Mismatches 2; Indels
                                                                                                                             Length 19;
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US-10-741-600-73758
US-10-741-600-73758
; Sequence 73759, Application US/10741600
; Publication No. US20050026169A1
; FRERRAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
                                                                                                            Score 11.8; DB 22;
Pred. No. 2.9e+04;
A. Mismatches 2;
                                                                                                                             Query Match 59.0%; Score 11.8; DE Best Local Similarity 86.7%; Pred. No. 2.98+Matches 13; Conservative 0; Mismatches
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ORGANISM: Artificial Sequence
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      FEATURE:
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US-10-888-226-46/C

Sequence 46, Application US/10888226

Sequence 46, Application US/10888226

Sequence 46, Application US/10888226

Sequence 46, Application US/10888226

Sequence 46, Application US20050124568A1

GENERAL INFORMATION:
APPLICANT: McSwiggen, James

APPLICANT: MCSwiggen, USman, Nassim

TITLE OF INVENTION: GNOE Expression Using Short Interfering Nucleic Acid (siNA)

TITLE OF INVENTION: GNOE Expression Using Short Interfering Nucleic Acid (siNA)

CURRENT APPLICATION NUMBER: US/10/888,226

CURRENT FILING DATE: 2004-01-1

PRIOR PELING DATE: 2003-07-11

PRIOR PELING DATE: 2004-04-16

PRIOR PELING DATE: 2004-04-16

PRIOR PELING DATE: 2004-01-14

PRIOR PELING DATE: 2004-01-14

PRIOR PELING DATE: 2003-11-24

PRIOR PILING DATE: 2003-11-24

PRIOR PILING DATE: 2003-11-24

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58.0%; Score 11.6; DB 21; Length 18; 77.8%; Pred. No. 3.7e+04; ive 0; Mismatches 4; Indels (
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                                                                                                                                                                                                                                                                                                                                                       Sequence 31, Application US/09768436;
Patent No. US20020006639A1
GENERAL INFORMATION:
APPLICANT: Paul Andrew Whittaker et al
FILE OF INVENTION: Disease-Associated Gene
FILE REFERENCE: Case No. US2002006633A1 4-31306A/HO 25;
CURRENT APPLICATION NUMBER: US/09/768,436;
UNWBER OF SEQ ID NOS: 70
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 31
LENGTH: 19
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Gaps

; 0

Indels

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GENERAL INFORMATION:
APPLICANT: Ian Popoff
APPLICANT: Jacqueline Wyatt
TITLE OF INVENTION: BXPRESSION
FILE REFERENCE: RTS-0182.
CURRENT APPLICATION NUMBER: US/09/731,457B
CURRENT FILING DATE: 2000-12-06
SEQ ID NOS: 87
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 11.6; DB 9;
Pred. No. 3.7e+04;
                61.1%; Pred. No. 3.7e+04;
tive 3; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTHER INFORMATION: Antisense Oligonucleotide US-09-731-457B-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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ORGANISM: Artificial Sequence
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Best Local Similarity 77.8%;
Matches 14; Conservative
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                                                                                                             1 GACCGCATAGACTTCTCA
                                                11; Conservative
                Best Local Similarity
Matches 11; Conserva
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US-09-731-457B-14
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US-10-345-092-51
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| Sequence 460, Application US/1088226
| Sequence 460, Application No. US20050124568A1
| GENERAL INFORMATION: Herapeutics, Inc. |
| APPLICANT: Sirrar Therapeutics, Inc. |
| APPLICANT: Weswiggen, James |
| TITLE OF INVENTION: Rea Expression Using Short Interfering Nucleic Acid (siNA) |
| TITLE OF INVENTION: Gene Expression Using Short Interfering Nucleic Acid (siNA) |
| TITLE OF INVENTION: Gene Expression Using Short Interfering Nucleic Acid (siNA) |
| TITLE OF INVENTION: Gene Expression Using Short Interfering Nucleic Acid (siNA) |
| TITLE OF INVENTION: Gene Expression Using Short Interfering Nucleic Acid (siNA) |
| TITLE OF INVENTION: Gene Expression Using Short Interfering Nucleic Acid (siNA) |
| TITLE OF INVENTION: Gene Expression Using Short Interfering Nucleic Acid (siNA) |
| TITLE OF INVENTION NUMBER: US 60/486,729 |
| PRIOR FILING DATE: 2003-07-11 |
| PRIOR PELICATION NUMBER: US 10/720,448 |
| PRIOR PELICATION NUMBER: US 10/720,448 |
| PRIOR PELICATION NUMBER: US 10/30,650 |
| PRIOR PELICATION NUMBER: PCT/US03/05028 |
| PRIOR PELICATION NUMBER: PCT/US03/05028 |
| PRIOR PELICATION NUMBER: E2003-02-20 |
| PRIOR APPLICATION NUMBER: US 60/358580 |
| PRIOR PELING DATE: 2003-02-20 |
| PRIOR PELICATION NUMBER: US 60/358580 |
| PRIOR APPLICATION NUMBER: US 60/358580 |
| PRIOR APPLICATION NUMBER: US 60/358580 |
| PRIOR APPLICATION NUMBER: US 60/358580 |
| PRIOR PELING DATE: 2003-02-20 |
| PRIOR PELING DATE: 2003-02-20 |
| PRIOR PELICATION NUMBER: US 60/358580 |
| PRIOR PELING DATE: 2003-02-20 |
| PRIOR 
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PRIOR APPLICATION NUMBER: US 10/444,853
PROR FILING DATE: 2003-05-23
PRIOR PILING DATE: 2003-05-23
PRIOR PILING DATE: 2003-02-20
PRIOR PILING DATE: 2003-02-20
PRIOR PILING DATE: 2003-02-20
PRIOR PILING DATE: 2003-02-20
PRIOR PRIOR PRIOR DATE: 2002-02-20
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 955
SOPTWARE: Patentin Version 3.3
SEQ ID NO 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR PILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: PCT/US03/05028
PRIOR FILING DATE: 2003-02-20
PRIOR PLILING DATE: 2003-02-20
PRIOR PILING DATE: 2002-02-20
Remaining Prior Application data removed - See File Wrapper or PALM.
WUMBER OF SEQ ID NOS: 955
SOFTWARE: Patent In version 3.3
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Pred. No. 3.7e+04;
0; Mismatches 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: RNA
ORGANISM: Artificial Sequence
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Best Local Similarity 77.8%;
Matches 14; Conservative
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Gaps

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Length 20; Indels

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APPLICANT: Vlaams Interuniversitair Instituut voor Biotechnol
TITLE OF INVENTION: No. US20030165506Alel alpha-catenin expressed in heart and testis
FILE REFERENCE: FVR/ATC/V067
CURRENT APPLICATION NUMBER: US/10/345,092
CURRENT FILING DATE: 2003-01-13
PRIOR APPLICATION NUMBER: 02002472.7
PRIOR APPLICATION NUMBER: 02 60/218,309
PRIOR FILING DATE: 2000-07-14
NUMBER OF SEQ ID NOS: 134
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 5:
LENGTH: 20
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RESULT 22

DB 22; Length 19

58.0%; Score 11.6;

Query Match

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Gaps
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                                                                                                                                                                                                                                                                                                                         Length 17;
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Pred. No. 4.7e+04;
4; Mismatches 1;
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Pred. No. 4.8e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 43, Application US/09795686;
Patent No. US20020094954A1
GENERAL INFORMATION:
APPLICANT: Stefansson, Hreinn
APPLICANT: Stefansson, Hreinn
APPLICANT: Gilcher, Jeffrey R.;
APPLICANT: Gilcher, Jeffrey R.;
TITLE OF INVENTION: HUWAN SCHIZOPHRENIA GENE;
FILE REFRENCE: 2345,2005-001;
CURRENT APPLICATION NUMBER: US/09/795,686;
CURRENT APPLICATION NUMBER: US 09/515,715;
PRIOR FILING DATE: 2001-02-28;
PRIOR FILING DATE: 2000-02-28;
NUMBER OF SEQ ID NOS: 1531
SOFTWARE: FastSEQ for Windows Version 4.0
: EBNGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Stefansson, Hreinn
APPLICANT: Stefansson, Hreinn
APPLICANT: Steinthorsdottir, Valgerdur
APPLICANT: Gulcher, Jeffrey, TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE
FILE REFERENCE: 2345.2004-001
CURRENT APPLICATION NUMBER: US/09/795,668
CURRENT APPLICATION NUMBER: 2001-02-28
PRIOR FILING DATE: 2000-02-28
PRIOR FILING DATE: 2000-02-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
; TITLE OF INVENTION: Levels of NF-Kappa B; FILE REFERENCE: 400/022 (MBHB00-612-D)
; CURRENT APPLICATION NUMBER: uS/09/864,785; CURRENT FILING DATE: 2001-05-23
; NUMBER OF SEQ ID NOS: 3929
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 2881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 1531
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 43
LENGTH: 20
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Patent No. US20020045577A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                            57.0%;
61.5%;
                                                                                                                                                                                         TYPE: RNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 57.0%;
Best Local Similarity 92.3%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                     6 CATAGACTICICA 18
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                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 61.5
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
CORGANISM: Homo sapiens
US-09-795-668-43
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US-09-795-686-43
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                                                                                                                                                                                                                                       FEATURE:
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Sequence 2881, Application US/09864785

Sequence 2881, Application US/09864785

Sequence 2881, Application US/09864785

GENERAL INFORMATION:

APPLICANT: Rinchoomb, Dan

APPLICANT: Draper, Ken

APPLICANT: Draper, Ken

APPLICANT: McSwiggen, Jim

TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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Pred. No. 4.7e+04;
                         Sequence 289, Application US/10056414
Publication No. US20030003469A1
GENERAL INFORMATION:
APPLICANT: Stinchcomb, Dan T.
Draper, Kenneth G.
MCSwiggen, James
TITLE OF INVENTION: RIBOZYME TREATMENT OF
DISEASES OR COUNTIONS
RELATED TO LEVELS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US/10/056,414
FILING DATE: 23-Jan-2002
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/291,932A
FILING DATE: August 15, 1994
APPLICATION NUMBER: 08/245,466
FILING DATE: May 18, 1994
APPLICATION NUMBER: 07/987,132
FILING DATE: December 7, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM Compatible
OPERATINE SYSTEM: IBM P.C. DOS 5.0
SOFFWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/157
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 289:
                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 830
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 289:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 61.5%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                           CITY: Los Angeles
STATE: California
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ZIP: 90071-2066
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           US-10-056-414-289
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92.3%; Pred. No. 4.8e+04;
tive 0; Mismatches 1
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                                                             8 TAGACTTCTCAGA 20
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Matches 12, Conservative
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  Best Local Similarity 92.3
Matches 12; Conservative
                                                                                                     17 regacricicada 5
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Best Local Similarity
Matches 12; Conserva
                                                                                                                                                                     RESULT 28
US-10-148-806-21
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; Publication No. US20030138933A1
; GRERRAL INFORMATION:
   APPLICANT: Bai. Chang
   APPLICANT: Liu, Xiaomei
   APPLICANT: Dane MOLECULES ENCODING HUMAN NHL, A DNA
   TITLE OF INVENTION: UNBER: US/10/148,806
   CURRENT APPLICATION NUMBER: US/00/33065
   PRIOR PILING DATE: 2000-12-09
   PRIOR FILING DATE: 1999-12-09
   NUMBER OF SEQ ID NOS: 38
   SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57.0%; Score 11.4; DB 15; Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 11.4; DB 9; Length 20;
Pred. No. 4.8e+04;
0; Mismatches 1; Indels
                                                                  Length 20;
                                                                                                            1; Indels
                                                               Score 11.4; DB 9;
Pred. No. 4.8e+04;
                                                                                                                                                                                                                                                                                        Sequence 10,743
Sequence 10,743
Fatent No. US200201651441
GENERAL INFORMATION:
APPLICANT: Stefanson, Hreinn
APPLICANT: Stefanson, Hreinn
APPLICANT: Gulcher, Jeffrey R.
TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE
FILE REFERENCE: 2345.2004-001
CURRENT APPLICATION NUMBER: US/09/946,807
CURRENT APPLICATION NUMBER: US/09/946,807
CURRENT APPLICATION NUMBER: US/09/795,668
FRIOR APPLICATION NUMBER: US/09/795,668
FRIOR PILING DATE: 2001-02-28
FRIOR FILING DATE: 2000-02-28
NUMBER OF SEQ ID NOS: 1531
SOFTWARE: FREASEQ for Windows Version 4.0
SEQ ID NO 43
LENGTH: 20
                                                                                                            0; Mismatches
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ORGANISM: Artificial Sequence
                                                                  57.0%;
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Best Local Similarity 92.3
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 GCATAGACTTCTC 17
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                                                           Ouery Match
Best Local Similarity 92.3
Matches 12; Conservative
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; ORGANISM: Homo sapiens
US-09-795-686-43
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US-10-148-806-20/c
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US-09-946-807-43
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Query Match

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US-10-174-319-35/c
$ Sequence 35, Application US/10174319
$ Sequence 35, Application US/10174319
$ Publication No. US20030232771A1
$ GENERAL INFORMATION:
$ APPLICANT: Donna T. Ward
$ APPLICANT: Kenneth W. Dobie
$ TITLE OF INVENTION: AWTISENSE MODULATION OF MARK3 EXPRESSION
$ FILE REFERENCE: PTS-0018
$ CURRENT APPLICATION NUMBER: US/10/174,319
$ CURRENT FILING DATE: 2002-06-17
$ NUMBER OF SEQ ID NOS: 121
$ SEQ ID NO 35
$ LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 20;
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Sequence 21, Application US/10148806
Publication No. US20030138933A1
GENERAL INFORMATION:
APPLICANT: Bai, Chang
APPLICANT: Liu, Xiaomei
TITLE OF INVENTION: DNA MOLECULES ENCODING HUMAN NHL, A DNA
FILE REFERENCE: 20585P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57.0%; Score 11.4; DB 15; 92.3%; Pred. No. 4.8e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ) OTHER INFORMATION: Antisense Oligonucleotide US-10-174-319-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/10/148,806
CURRENT FILING DATE: 2002-06-05
PRIOR APPLICATION NUMBER: US00/33065
PRIOR FILING DATE: 2000-12-09
PRIOR APPLICATION NUMBER: 60/169,970
PRIOR FILING DATE: 1999-12-09
NUMBER OF SEQ ID NOS: 38
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 21
LENGTH: 20
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CTHER INFORMATION: Antisense compound US-10-831-901A-2082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Artificial Sequence
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92.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 ATAGACTTCTCAG 19
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Best Local Similarity 92.3
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13 ACAGACTTCTCAG 1
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Pred. No. 4.8e+04;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 57.0%; Score 11.4; DB 19; Length 20; Best Local Similarity 92.3%; Pred. No. 4.8e+04; Matches 12; Conservative 0; Mismatches 1; Indels
                                                                                                                 APPLICANT: Susan M. Preier APPLICANT: Kenneth W. Dobie TITLE OF INVENTION: ANTISENSE MODULATION OF MARK3 EXPRESSION FILE REFERENCE: PTS-0018
CURRENT APPLICATION MUBBER: US/10/174,319
CURRENT FILING DATE: 2002-06-17
NUMBER OF SEQ ID NOS: 121
SEQ ID NO 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 24, Application US/10304111
; Publication No. US20040102403A1
; Publication No. US20040102403A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: MODULATION OF FIBRILLARIN EXPRESSION
; FILE REFERENCE: HTS-0075
; CURRENT APPLICATION NUMBER: US/10/304,111
; CURRENT FILING DATE: 2002-11-21
; NUMBER OF SEQ ID NOS: 71
; SEQ ID NO 24

LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Antisense Oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 32
US-10-831-901A-2082/C
Sequence 2082, Application US/10831901A
Publication No. US20050100885A1
GENERAL INFORMATION:
APPLICANT: Crooke, Stanley T.
APPLICANT: Ecker, David J.
APPLICANT: Sampath, Rangarajan
APPLICANT: Hosteration Massire, Christian
APPLICANT: Hosteradler, Steven A.
APPLICANT: Hosteradler, Steven A.
APPLICANT: Lowery, Kristin Sannes
                                        Sequence 101, Application US/10174319
Publication No. US20030232771A1
GENERAL INFORMATION:
APPLICANT: Donna T. Ward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 92.3%;
Matches 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 radacarcrcada 14
                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: H. sapiens
                                                                                                                                                                                                                                                                                                                                                                                         US-10-174-319-101
RESULT 30
US-10-174-319-101
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Sequence 2003, Application US/10831901A

Publication No. US20050100885A1

GENERAL INFORMATION:
APPLICANT: Ecker, David J.
APPLICANT: Sampath, Rangarajan
APPLICANT: Refer, Stann M.
APPLICANT: Hofstaller, Steven A.
APPLICANT: Hofstaller, Steven A.
APPLICANT: Baster, Erries Sannes
APPLICANT: Bennett, C. Frank
APPLICANT: Bennett, C. Frank
TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
TITLE OF INVENTION: Compositions (SARS)
CURRENT APPLICATION NUMBER: US/10(811,901A)
CURRENT FILING DATE: 2004-04-26
CURRENT FILING DATE: 2004-04-26
CURRENT FILING DATE: 2004-04-26
APPLICANT: Baker, Brenda F.

APPLICANT: Bennett, C. Frank
TITLE OF INVENTION: Compositions And Methods For The Treatment of Severe
TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
TITLE OF INVENTION: Acute Respiratory Syndrome (SARS)
FILE REFERENCE: ISISO083-100 (BIOLO008US)
CURRENT APPLICATION NUMBER: US/10/831,901A
CURRENT FILING DATE: 2003-04-26
PRIOR APPLICATION NUMBER: 60/466,426
PRIOR APPLICATION NUMBER: 60/468,562
PRIOR PILING DATE: 2003-05-06
PRIOR FILING DATE: 2003-05-06
PRIOR PILING DATE: 2003-05-06
PRIOR PILING DATE: 2003-05-06
PRIOR APPLICATION NUMBER: 60/477,637
PRIOR APPLICATION NUMBER: 60/477,637
PRIOR APPLICATION NUMBER: 60/483,579
PRIOR APPLICATION NUMBER: 60/483,579
PRIOR PILING DATE: 2003-06-27
NUMBER OF SEQ ID NOS: 30063
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2082
LENGTH: 200
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Pred. No. 4.8e+04;
0; Mismatches 1;
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PRIOR APPLICATION NUMBER: 60/466,426
PRIOR FILING DATE: 2003-04-28
PRIOR PRIOR PRICE: 2003-06-06
PRIOR FILING DATE: 2003-05-06
PRIOR APPLICATION NUMBER: 60/468,562
PRIOR APPLICATION NUMBER: 60/467,770
PRIOR APPLICATION NUMBER: 60/468,627
PRIOR PLING DATE: 2003-05-06
PRIOR PLING DATE: 2003-06-06
PRIOR PLING DATE: 2003-06-10
PRIOR APPLICATION NUMBER: 60/477,637
PRIOR PLING DATE: 2003-06-10
PRIOR PLING DATE: 2003-06-27
NUMBER OF SEQ ID NOS: 30063
SOFTWARE: FRALSEQ for Windows Version 4.0
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Query Match
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                                                                                                                                                                                                                                                                      Score 11.4; DB 21; Length 20;
Pred. No. 4.8e+04;
0; Mismatches 1; Indels
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2084, Application US/10831901A
Publication No. US20050100885A1
GENERAL INFORMATION:
APPLICANT: Crooke, Stanley T.
APPLICANT: Ecker, David J.
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Sequence 2085, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
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                                                                                                                                                       ; OTHER INFORMATION: Antisense compound US-10-831-901A-2083
                                             TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                      57.0%;
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Best Local Similarity 92.3
Matches 12; Conservative
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Best Local Similarity 92.3
Matches 12; Conservative
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SEQ ID NO 2084
LENGTH: 20
LENGTH: 20
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APPLICANT: Crooke, Stanley T.
APPLICANT: Crooke, Stanley T.
APPLICANT: Ecker, David J.
APPLICANT: Ecker, Sampath, Rangarajan
APPLICANT: Freier, Susan M.
APPLICANT: Massire, Christian
APPLICANT: Massire, Christian
APPLICANT: Lowery, Kristin Sannes
APPLICANT: Swayze, Eric
APPLICANT: Banet, C. Frank
APPLICANT: Banet, C. Frank
TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
TITLE OF INVENTION: Compositions And Methods For The Treatment
FILLS OF INVENTION: Compositions And Methods For The Treatment Of Severe
CURRENT APPLICATION NUMBER: US/10/831,901A
CURRENT APPLICATION NUMBER: US/10/831,901A
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Pred. No. 4.8e+04;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Antisense compound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/466,426
PRIOR FILING DATE: 2003-04-28
PRIOR APPLICATION NUMBER: 60/468,562
PRIOR FILING DATE: 2003-05-06
PRIOR APPLICATION NUMBER: 60/467,770
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PRIOR APPLICATION NUMBER: 60/468,627
Massire, Christian
Hofstadler, Steven A.
Lowery, Kristin Sannes
Swayze, Eric
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ORGANISM: Artificial Sequence
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Matches 12; Conservative
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US-10-831-901A-2086/c
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APPLICANT: Ecker, David J.
APPLICANT: Ecker, David J.
APPLICANT: Ecker, David J.
APPLICANT: Ecker, David J.
APPLICANT: Sampath, Rangarajan
APPLICANT: Massire, Christian
APPLICANT: Cowney, Kristin Sannes
APPLICANT: Cowney, Kristin Sannes
APPLICANT: Cowney, Campositions And Methods For The Treatment Of Severe
ITILE OF INVENTION: Compositions And Methods For The Treatment Of Severe
ITILE OF INVENTION: Acute Respiratory Syndrome (SARS)
FILE REFERENCE: ISISO083-100 (BIOL0008US)
CURRENT FILING DATE: 2003-04-04-26
PRIOR FILING DATE: 2003-04-20
PRIOR APPLICATION NUMBER: 60/466,426
PRIOR PELING DATE: 2003-04-30
PRIOR PELING DATE: 2003-04-30
PRIOR PELING DATE: 2003-06-10
PRIOR PELING DATE: 2003-06-10
PRIOR PELING DATE: 2003-06-10
PRIOR APPLICATION NUMBER: 60/468,527
PRIOR PELING DATE: 2003-06-10
PRIOR APPLICATION NUMBER: 60/463,579
PRIOR APPLICATION NUMBER: 60/463,579
PRIOR PELING DATE: 2003-06-27
NUMBER OF SEQ ID NOS: 30063
SOFTWARE: PESELSEQ for Windows Version 4.0
SEQ ID NO 2087
LEAST STANDARD
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Pred. No. 4.8e+04;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                Score 11.4; DB 21; Length 20;
Pred. No. 4.8e+04;
0; Mismatches 1; Indels
PRIOR APPLICATION NUMBER: 60/477,637
PRIOR FILING DATE: 2003-06-10
PRIOR PILICATION NUMBER: 60/483,579
PRIOR PILING DATE: 2003-06-27
NUMBER OF SEQ ID NOS: 30063
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2086
LENGTH: 20
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CTHER INFORMATION: Antisense compound
US-10-831-901A-2086
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                                                                                                                                                                                                         TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity 92.3%;
Matches 12; Conservative
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Best Local Similarity 92.3
....hes 12; Conservative
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Sequence 20, Application US/10859792

Sequence 20, Application US/10859792

Publication No. US20050136425A1

GENERAL INFORMATION:

APPLICANT: Bai, Chang

APPLICANT: Liu, Xiaomei

TITLE OF INVENTION: DNA MOLECULES ENCODING HUMAN NHL, A DNA

TITLE OF INVENTION: HELICASE

CURRENT APPLICATION NUMBER: US/10/859,792

CURRENT APPLICATION NUMBER: US/10/148,806

PRIOR FILING DATE: 2002-06-03

PRIOR FILING DATE: 2000-12-09

PRIOR FILING DATE: 2000-12-09

PRIOR FILING DATE: 2000-12-09

PRIOR FILING DATE: 1999-12-09

PRIOR FILING DATE: 1999-12-09

NUMBER OF SEQ ID NOS: 38

SOFTWARE: FastSEQ for Windows Version 4.0

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57.0%; Score 11.4; DB 21; Length 20; 92.3%; Pred. No. 4.8e+04; tive 0; Mismatches 1; Indels
PRIOR FILING DATE: 2003-04-28
PRIOR APPLICATION NUMBER: 60/468,562
PRIOR FILING DATE: 2003-05-06
PRIOR PILING DATE: 2003-05-06
PRIOR APPLICATION NUMBER: 60/467,770
PRIOR PILING DATE: 2003-04-30
PRIOR FILING DATE: 2003-06-06
PRIOR FILING DATE: 2003-06-10
PRIOR FILING DATE: 2003-06-10
PRIOR FILING DATE: 2003-06-10
PRIOR FILING DATE: 2003-06-10
PRIOR FILING DATE: 2003-06-27
NUMBER OF SEQ ID NOS: 30063
SOFTWARE: PSELSEQ for Windows Version 4.0
SEQ ID NO 2089
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COTHER INFORMATION: Antisense compound
US-10-831-901A-2089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ) OTHER INFORMATION: oligonucleotide US-10-859-792-20
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity 92.3
Matches 12; Conservative
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Best Local Similarity
Matches 12; Conserva
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US-10-859-792-20/c
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Search completed: August 12, 2005, 12:19:44 Job time : 376 secs

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41.0 19 8 AZ436629 41.0 19 8 AZ454430 41.0 19 8 AZ647364 41.0 19 8 AZ647364	12 9 8	0000	0 119 8 8 8 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	20 19 9	2000	17 9	1199	0000	200	2002	20 8	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	200	0 11 0	0 18 4	0 1 18 9	1000	186	110	50 7	20 70 70 70 70 70 70 70 70 70 70 70 70 70	20 B	20 8	20 8	2000	0 20 8	0 13 9	14 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	917	71.	0.00
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5.1.6 Compugen Ltd.		ch time 1779 Seconds out alignments) 29 Million cell updates/sec			. sən	8: 12452								4	result being stribution.												AZ440002 $1M0230\overline{E}19$ AJ648088 AJ648088				
GenCore version 5.1. Copyright (c) 1993 - 2005 Com	- nucleic search, using sw model	August 12, 2005, 11:03:34 ; Search t (without 427.929 M	US-09-743-825-10 re: 20 1 qaccqcataqacttctcaga 20	e: Ga	344 Be	r of hits satisfying chosen parameters	seq length: 0 seq length: 20	Minimum Match Maximum Match	Listing first 100 summaries EST:*		3: 95-hc:* 4: gb-hc:* 4: gb-est3:*			9: gb_gss2:*	NO. IS the number of results predicted by greater than or equal to the score of the is derived by analysis of the total score di	•	* Query	re Match Length DB	51.0 19 7 49.0 19 8	.6 48.0 20.8 .2 46.0 17 9	45.0 18 5 45.0 19 1	45.0 19 9 45.0 20 9	.8 44.0 16 5 8 44.0 19 8	8 44.0 20 9	.8 44.0 20 9 .6 43.0 16 1	.6 43.0 19 8 .6 43.0 20 7	8.6 43.0 20 8 AZ440002 8.4 42.0 17 1 AJ648088	4 42.0 19 8	.4 42.0 19 8 .4 42.0 20 8	.2 41.0 16 9	.2 41.0 19 1 .2 41.0 19 8
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/lab host-"E. Coli strain XL10-Gold, T1-resistant, F."
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/clone_lib="Wouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42IV; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources/documents/dhares/). The DNA
was bydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophorasis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AR129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XI10-Gold (Stratagene) cells
and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                             Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 19)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weise, R., Dunse whole genome scaffolding with paired end reads from 10kb plasmid inserts
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                                                                                                                                                                                                                                                                                                                                                                                 Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0016 row: E column: 23
Seq primer: CGTTGTAAAACGACGACCAGT
Class: plammid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Mus musculus"
/mol_type="genomic DNA"
/ktrain="c57BL/64"
/db xref="taxon:10090"
/clone="UUGCIM0016E23"
                                                                                                                                                                                                                                        Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           High quality sequence stop: 19.
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:8296"
/db_xref="taxon:8296"
/tisaue_type="Neural Tube, Notochord, Somites"
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/cell_type="Includes Neural tube (NT)"
/dev_stage="Stage=18-22 Neural tube (NT)"
/clone_lib="Stl8-22 Neural tube (NT)"
/note="Vector: pCNVSport6; Site_1: Not1; Site_2: Sall;
/note="Vector: pCNVSport6; Sacterial host is EMDHIOB="CONA, Average insert size is 1.5 kB.
TAG_LIB=NT"
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BM397569 5009-0-34
BM399684 5009-0-60
C01992 HUMGS000401
                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukāryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Caudata; Salamandroidea; Ambystomatidae;
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Max Planck Institute of Molecular Cell Biology and Genetics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfotenhauerstrasse 108,01307 Dresden, Germany Tel: 0049 351 210 2620
Fax: 0049 351 210 1489
Email: tanaka@mpi-cbgde
Blate: NT014C row: 10 column: A
Seq primer: GCA CAT TAG GCC TAT TTA GGT GAC A.
Location/Qualifiers
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Contact: Elly M. Tanaka
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Mus musculus (house mouse)
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S015504-024-025-M13-SP6 MPIZ-ADIS-024-developing root Beta vulgaris CDNA clone 024-025-M13 5-PRIME, mRNA sequence.
B0593906.1 G1:26123489
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
1 (bases 1 to 18)
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes Plant J. 32 (5), 845-857 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:54126"
/clone lib="Mixed stage fosmid library of P. pacificus
var. California"
/note="Vector: pEpifos-5 Fosmid vector"
                       Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.

1 (bases 1 to 17)
Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
AppaDB: an AcedB database for the nematode satellite organism
Pristionchus pacificus
Nucleic Acids Res. 32 (1), D421-D422 (2004)
Contact: Sommer RJ
                                                                                                                                                                                                                                                                                                                                                                                                              Email: raif.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
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ADIS DNA core facility at MPIZ
ADIS DNA core facility at MPIZ
MAx.Planck-Institute for Plant Breeding Research
Carl-von_Linne Weg 10, 50829 Koeln, Germany
Fax: 049221506281
Fmail: weisshaw@mpiz-koeln.mpg.de
Insert Length: 18 Std Brror: 0.00
Plate: 25 row: M column: 13
Seg primer: SP6; CATACGATTTAGGTGACCTATAG.
Location/Qualifiers
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Max-Planck-Institute for Developmental Biology
Spemanustr. 37-39, Tuebingen D-72076, Germany
Fax: 00497071601371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
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Pred. No. 4.8e+06;
0; Mismatches 3;
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Location/Qualifiers
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Matches 11; Conservative
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           Eukaryota; Buteleostomi; Bukaryota; Buteleostomi; Bukaryota; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus. 1 (bases 1 to 20)

Standaria; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus. 1 (bases 1 to 20)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von Niederhausern, and Wright, D., Weiss, R. Unpublished (2000)

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah Genome Center
University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 B., SLC, UT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gil4732114[gb]AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli Xil0-Gold (Stratagene) cells and selected for ampicillin resistance."
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17 bp DNA linear GSS 09-JUL-2004 PR10130b G06 2 - PRI0130b BR (17) Mixed stage fosmid library of P. pacificus var. California Pristionchus pacificus genomic, genomic survey sequence.
CL681189.1 GI:50188197
GSS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /sex="Male"
/lab host="B. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Insert Length: 10000 Std Error:
Plate: 0538 row: G column: 04
Seq primer: CGTYCTAAAACGACGGCCAGT
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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:10090"
/clone="UUGC1M0538G04"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                High quality sequence stop: 20.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: 801 585 5606
Fax: 801 585 7177
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Best Local Similarity
Matches 12; Conserva
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source

FEATURES

RESULT 4 CL681189/c LOCUS DEFINITION

ORIGIN

ACCESSION

VERSION KEYWORDS

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Gaps

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Pan troglodytes DNA, clone: RP43-061K12.T7, genomic survey
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
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Pristionchus pacificus
Bukaryota, Metazoa, Nematoda, Chromadorea, Diplogasterida,
Bukaryota, Metazoa, Nematoda, Chromadorea, Diplogasterida,
1 (bases 1 to 19)
Srinivasan, J., Otto, G.W., Kahlow, U., Geisler, R. and Sommer, R.J.
AppabB: an AcedB database for the nematode satellite organism
Pristionchus pacificus
Nucleic Acids Res. 32 (1), D421-D422 (2004)
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/clone lib="Mixed stage fosmid library of P. pacificus
var. California"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
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6.3e+06;
... 5; Indels
                                  Indels
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Max-Planck-Institute for Developmental Biology
Spenannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371

    19
/organism="Pristionchus pacificus"

   100.0%; Pred. No. 6.3e+06;
tive 0; Mismatches 0;
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0; Mismatches
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/strain="California"
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AG188131.1 GI:45220300
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Best Local Similarity 70.6%;
Matches 12; Conservative
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Class: fosmid ends.
      Best Local Similarity 100.
Matches 9; Conservative
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ORGANISM
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VERSION
KEYWORDS
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TITLE
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KEYWORDS
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CL671780
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AG188131
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Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred
V0.020425.c. Vector identified by cross_match with the -minscore 20
and -minmatch 12 options. Vector: pBlueScriptil(SK+) R. Site 1:
ECORI R. Site 2: NotI 5' Seq primer M13F Description: Normalised
library constructed from Bovine Uterus tissue. Clones available
from UK Centre for Functional Genomics in Farm Animals, Roslin
Institute, Roslin, Midlothian, UK, EH25 9PS, www.arkgenomics.org.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 19)
Anderson, S. T., Finlayson, H.A. and Archibald, A.L.
Anderson, S. T., Finlayson, H.A. and Archibald, A.L.
Development of colfs and EST resources for studying reproduction and embryo development in pigs and cattle
Unpublished (2004)
Contact: Anderson SI
Genomics and Bioinformatics
                                                                                                                                                                                                                                                                                                                                    /note="Vector: pcWvSPORT6; Site_1: Sal1; Site_2: Not1;
CODA library from sugar beet, library provided by KWs
Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sal1-Not1, primer sites and
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/mol_type="mRNA"
/mol_type="mRNA"
/db_xref="taxon:9913"
/clone="KN224-006 N20"
/tissue_type="uterus"
/clone_lib="KN224"
/clone_lib="KN224"
/clone_lib="KN224"
/clone_lib="KN224"
/clone_lib="KN224"
/clone_lib="KN234"
/cl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SP6-Sal1-CCACGCGTCCG-Sprime-cDNA-polyA-CC-Not1-T7; Note:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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0
                                                                                                                                                                                                                                    /tissue type="developing root"
/lab host="EMDH10B"
/clone_lib="MPIZ-ADIS-024-developing root"
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                                                                                                                                                                         'db_xref="taxon:161934"
                                                                                                                               db_xref="GABI:192944"
                                                                                                                                                                                                        clone="024-025-M13"
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Best Local Similarity 70.6*
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REFERENCE AUTHORS

TITLE

COMMENT

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RESULT 6

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/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"/clone_lib="Mouse 10kb plasmid UUGC1M library"
/mol_type="mRNA"
/culfivar="KWS2320 (double haploid, monogerm breeding
                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             44.0%; Score 8.8; DB 5;
83.3%; Pred. No. 7.8e+06;
ive 0; Mismatches 2;
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Seg primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
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                                                           db_xref="GABI:184446"
|db_xref="taxon:161934"
|clone="024-008-E21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="UUGC1M0391L22"
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Location/Qualifiers
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
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EOSB3512
E0585512
                      Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C.J.,
Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C.J.,
Hoon, S.T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H.
Direct Submission
Submitted (07-JAN-2002) Hong-Seog Park, Korea Research Institute of
Bioscience and Biotechnology (KRIBB), Genome Research Center (GRC);
Bioscience and English (RRBD), Genome Research Center (GRC);
Tel:82-42-866-7181, Fax:82-42-860-4409)
Clones are derived from the chimpanzee BAC library RP-43 This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.
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1 (Bases I to 16)
Herwig, R., Schulz, B., Weisshaar, B., Hennig, S., Steinfath, M., and Radelof, U.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes Plant J. 32 (5), 845-857 (2002)
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/cell_type="lymphocytes"
/clone_lib="RP-43 Chimpanzee Male BAC Library"
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ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Kosln, Germany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fax: 00492215062851
Email: weisehaa@mpiz-koeln.mpg.de
Insert Length: 16 Std Error: 0.00
Plate: 8 row: E column: 21
Seq primer: SP6; CATACGATTTAGGTGACATATAG.
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/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="RP43-061K12.T7"
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R.Site 1 : EcoRI
R.Site 2 : EcoRI.
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AZ585898 13-DEC-2000 1M0391L22F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0391L22 F, genomic survey sequence.
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Rose, M., Rose, M., Stokee, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                    Special-CCACGCGTCCG-Sprime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"
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University of Utah Genome Center
University of Utah
Windersity of Utah
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Winders Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
84112, USA
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Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C.J., Hoon, S.T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H. Direct Submitselon

Bioscience and Biotechnology (KRIBB), Genome Research Institute of Bioscience and Biotechnology (KRIBB), Genome Research Center (GRC); S., Oun-dong, Yusong-gu, Daejeon 305-33, Korea

[B-mail:redstonedmail.Kribb.re.kr, URL:http://phs.grc.kribb.re.kr/, Tel:82-42-866-7181, Pax:82-42-860-4409)

Clones are derived from the chimpanzee BAC library RP-43 This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.
                                                                                                                                                                                                                                                                                                                                                  AG200702 20 bp DNA linear GSS 06-MAR-2004
Pan troglodytes DNA, clone: RP43-082N04.TJ, genomic survey
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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/cell_type="lymphocytes"
/clone_lib="RP-43 Chimpanzee Male BAC Library"
/clone_lib="RP-43 Chimpanzee Male BAC Library'
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83.3%; Pred. No. 8.1e+06;
iive 0; Mismatches 2;
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/organism="Pan troglodytes"
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                                                                  (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gal electrophoresis. Vector DNA was prepared from a derivative of pwapt (gil 4732114 [gb] AP129072.1), a copy number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xil0-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hoon, S.T., Kim,Y., Kim,S., Han,Y., Woo,T., Park,K., Bun,C.J., Hoon,S.T., Chu,M., Kim,H., Joo,S., Kim,C., Song,W. and Yoo,H. Direct Submitseion

Direct Submitseion

Bibmitted (07-JAN-2002) Hong-Seog Park, Korea Research Institute of Bioscience and Biotechnology (KRIBB), Genome Research Center (GRC); S., Oun-dong, Yusong-gu, Daejeon 305-333, Korea

[E-mail:redstone@mail.Kribb.re.kr, UKL:http://phs.grc.kribb.re.kr/, Tel:82-42-866-7181, Fax:82-42-860-4409)

Clones are derived from the chimpanzee BAC library RP-43 This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.
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Pan troglodytes
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
                            musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
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     /note="Vector: PWD42nv; Purified genomic DNA from M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AG187931 20 bp DNA linear GSS 06
Pan troglodytes DNA, clone: RP43-061C23.TJ, genomic survey
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Pred. No. 8e+06;
0; Mismatches 2; Indels
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/mol_type="genomic DNA"
/db_xref="taxon:9598"
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/cell_type="lymphocytes"
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R.Site 1 : EcoRI
R.Site 2 : EcoRI.
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83.3%;
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CO783852 20 bp mRNA linear EST 05-AUG-2004 BL279A E02 6-Day Axolotl Tail Blastema (6DAxBL) Ambystoma mexicanum cDNA 5<sup>7</sup> similar to hypothetical protein, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lobases 1 to 20)
Habermann, B., Bebin, A.G., Herklotz, S., Volkmer, M., Eckelt, K., Pehlke, K., Epperlein, H.H., Schackert, H.K., Wiebe, G. and Tanaka, E.M. An Ambystoma mexicanum EST sequencing project: Analysis of 17,352 expressed sequence tags from embryonic and regenerating blastema
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Caudata; Salamandroidea; Ambystomatidae;
                                                                                                                                                                                                                                /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
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Tel: 0049 351 210 2620
Fax: 0049 351 210 1489
Email: tanaka@mpi-cbg.de
Plate: BL279A row: 02 column: E
Plate: 0012 row: E column: 23
Seg primer: CACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
                                                                                                        .. .19
organism="Mus musculus"
                                                                                                                                           /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                  /db_xref="taxon:10090"
/clone="UUGCIM0012E23"
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Contact: Elly M. Tanaka
                                                                              Location/Qualifiers
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Roslin, Midlochian, EH25 9PS, UNITED KINGDOM
Roslin, Midlochian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred
vo.020425.c. Vector identified by cross match with the -minscore 20
and -minmatch 12 options. Vector:pBlueScriptII(KS+) R. Sitel: ECCRI
R. Sitel: Noti 5' Seq Primer M13F Normalised library constructed
from pig uterus. Clones available from UK Centre for Functional
Genomics in Farm Animals, Roslin Institite, Roslin, Midlothian, UK,
EH25 9PS, www.arkgenomics.org.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AZ309116 19-20-2000 19 DNA linear GSS 29-SEP-2000 IM0012E23R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0012E23 R, genomic survey sequence.
                                                                                                 (bases 1 to 16)
Anderson, S.I., Finlayson, H.A. and Archibald, A.L.
Development of cDNA and EST resources for studying reproduction and Unpublished (2004)
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Musaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,

Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.

1 (bases 1 to 19)

1 (bases 1 to 19)

Munn, D., Advagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Miderhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="utērus"
/clone_lib="CSEQRAN04"
/note="Vector: pBlueScriptII(KS+); Site_l: EcoRI; Site_2:
Not1; Single pass sequencing. Normalised library
constructed from pig uterus."
                                                                                Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Suina; Suidae; Sus.
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Pred. No. 1e+07;
0; Mismatches 4; Indels
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Insert Length: 10000 Std Error: 0.00
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Sus scrofa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="mRNA"
/db_xref="taxon:9823"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="C0001805 G15"
                                                                                                                                                                                                                                    Contact: Anderson SI
Genomics and Bioinformatics
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      GI:49417177
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73.3%;
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Best Local 11, Conservative
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Fax: 801 585 7177
Email: ddunn@genet
                                               Sus scrofa (pig)
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      AJ684587.1
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was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymersae and T4 polymurcleotide kinase. Adaptor oligomucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coll X110-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anderson, S. T., Finlayson, H.A. and Archibald, A.L.
Development of CDNA and EST resources for studying reproduction and
embryo development in pigs and cattle
Unpublished (2004)
Contact: Anderson SI
Genomics and Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred
Single pass sequencing. Bases called and trimmed with phred
O.0204025.c. Vector identified by cross match with the -minscore 20
and -minmatch 12 options. Vector:pBlueScriptII(KS) R. Sitel: EcoRI
R. Site2: NotI S' Seq Primer MI3F Normalised library constructed
from pooled ovaries. Clones available from UK Centre for Functional
Genomics in Farm Animals, Roslin Institite, Roslin, Midlothian, UK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AJ648088 CSEQRAN19 Sus scrofa cDNA clone C0003263_J08, mRNA
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/clone_lib="CSEQRAN19"
/note="vector: pBlueScriptl1(KS+); Site_1: EcoRI; Site_2:
Not1; Single pass sequencing; Normalised library
constructed from pooled ovaries"
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
1 (bases 1 to 17)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43.0%; Score 8.6; DB 8; Length 20; 73.3%; Pred. No. 1e+07; ive 0; Mismatches 4; Indels
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Local Similarity 90.0%; Pred. No. 1.3e+07;
Les 9; Conservative 0; Mismatches 1; Indels
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Location/Qualifiers
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/db_xref="taxon:9823"
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Matches 11; Conservative
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                                                                                                                /mol type="maxx" |
/db xref="taxon:8296" |
/tlssue type="Tail Blastema" |
/cell type="Tail Blastema" |
/coll type="Tail Blastema" |
/coll type="Tegenerating tail Blastema (6DAXBL)" |
/clone lib="6-Day Axolotl Tail Blastema (6DAXBL)" |
/note="Vector: pGWVSport6; Site 1: Not1; Site 2: Sall; |
/normalized cDNA plasmid library prepared by Invitrogen.
Size fractionated mRNA was polydT primed and cloned into Not1-Sall site of pGWVSport6. Bacterial host is EMDH10B-TONA. Average insert size is 1.67 kB.
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T., Rellly, M., Rose, M., Rose, R., Stockes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (http://www.jax.org/resources/documents/dnares/). The DNA
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1M0230E19R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0230E19 R, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       43.0%; Score 8.6; DB 7; Length 20; 73.3%; Pred. No. 1e+07; ive 0; Mismatches 4; Indels
           r: GCA CAT TAG GCC TAT TTA GGT GAC A. Location/Qualifiers
                                                                                               /organism="Ambystoma mexicanum"
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Insert Length: 10000 Std Error: C
Bate: 0230 row: E column: 19
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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/mol_type="genomic DNA"
/strain="C57BL/6J"
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Location/Qualifiers
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Unpublished (2000)
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Fax: 801 585 7177
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Best Local Similarity
Matches 11; Conserv
                 Seg primer:
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Euteleostomi; Sus.

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Gaps

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GSS 14-DEC-2000

AZ313531/c LOCUS DEFINITION

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ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

REFERENCE AUTHORS JOURNAL

TITLE

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/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clon=lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWM942nv; Purified genomic DNA from M.
note="Vector: PWM942nv; Purified genomic DNA from M.
musculus G57BL/GJ (male) was obtained from the Jackson
Laboratory Mouse DNA Resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Nese, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weise, R.
                                                                                                                                       AZ663240
1M0542H18R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0542H18 R, genomic survey sequence.
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llarity 66.7%; Pred. No. 1.38+07;
Conservative 0; Mismatches 6; Indel8
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Insert Length: 10000 Std Error: 0.00
Plate: 0542 row: H column: 18
Seg primer: CACACAGGAAACAGCTAATGACC

    .19
    /organism="Mus musculus"
/mol type="genomic DNA"
/strain="C57BL/6J"

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Mupublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center
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High quality sequence stop: 19.
Location/Qualifiers
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/clone="UUGC1M0542H18"
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Fax: 801 585 7177
17 ATTTCTCAGA 8
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35 Junn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longarce, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Unpublished (2000)

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
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                                                                                                                                             A2313531 19 bp DNA linear GSS 29-SEP-2000 1M0029N07R Mouse 10kb plasmid UUGCIM library Mus musculus genomic cone UUGCIM0029N07 R, genomic survey sequence.
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/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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Fax: 801 585 7177
Email: ddunnagenetics.utah.edu
Insert Length: 10000 Std Error: 0.(
Plate: 0029 row: N column: 07
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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/strain="C57BL/6J"
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/clone="UUGC1M0029N07"
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Location/Qualifiers
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Best Local Similarity 90.v.
Best Local 9; Conservative
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1 GACCGCATAGACTICTCA 18

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ORIGIN

RESULT 20 AZ303578/c DEFINITION

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REFERENCE AUTHORS JOURNAL

COMMENT

TITLE

ACCESSION VERSION KEYWORDS SOURCE

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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwb42 (gi|4732114|gb|AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
University of Utah
Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
                                                                                                                                       AZ771437 Couse 10kb plasmid UUGCIM linear GSS 16-FEB-2001 1M0573P03R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0573P03 R, genomic survey sequence.
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Insert Length: 10000 Std Error: 0
Plate: 0573 row: P column: 03
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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/strain="C57BL/6J"
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Location/Qualifiers
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Fax: 801 585 7177
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19 AATTCTCAGA 10
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AZ771437/c
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AUTHORS
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Dunn,D., Aoyaqi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Nese,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weise,R.
                                                                                                                                          AZ303578 1085 29-SEP-200 ANA linear GSS 29-SEP-200 AMO003H07F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0003H07 F, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
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/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Wector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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Insert Length: 10000 Std Error: 0.00
Plate: 0003 row: H column: 07
Seg primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
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Location/Qualifiers
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/clone="UUGC1M0003H07"
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GSS.
GACAGGATATGACTCTCA 19
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Fax: 801 585 7177
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Query Match

ORIGIN

Best Loca Matches

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VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

TITLE

JOURNAL

COMMENT

DEFINITION

RESULT 22 CL423466 ACCESSION

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/clone_lib="NCI_CGAP_LUS"
//clone_lib="NCI_CGAP_LUS"
//note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; lst strand cDNA was prepared from neuroendocrine lung carcinoid, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo. "
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                            Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D.,
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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Dunn, D., Aoyaqi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Nelly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weise, R., Tingey, A., von Mouse, whole genome scaffolding with paired end reads from 10kb
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University of Utah Genome Center
University of Utah
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Erro
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Unpublished (2000)
Unpublished (1997)
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                                                                                                                                                                                   CL423466 1inear GSS 16-MAR-2004 0180557-03A1-C11 UniformMu MuTAIL Library Zea mays genomic clone 0180557-03A1-C11, genomic survey sequence.
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Unpublished (2003)
Contact: Donald R. McCarty
Plant Molecular and Cellular Biology Program
University of Floratida
PO 110690 Gainesville, FL 32611-0690, USA
Tel: 352-392-1928 x322
Email: drm@ufl.edu
Sequence Sequence flanking probable Mu insertion site in UniformMu
Line: 0180557-03, Primer set: A
Class: transposon insertion site.
Location/Qualifiers
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/clone="0180557-03A1-C11"
/clone="10180557-03A1-C11"
/clone="Uberonization of the control                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
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1 (bases 1 to 19)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
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Latshaw,S., Tan,B-.C., Settles,A.M. and McCarty,D.R. Sequence tagged transposon insertions from the UniformMu
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41.0%; Score 8.2; DB 9; Length 16;
Best Local Similarity 76.9%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 3; Indels
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/mol type="genomic DNA"
/strain="W22 (ACR, bz1-m9)"
/cultivar="UniformMu"
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SOURCE ORGANISM

AUTHORS TITLE

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AA916934/c

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Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (Dases 1 to 19)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longare, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weise, R.,
Mouse whole genome scaffolding with paired end reads from 10kb
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1M0256F21F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC1M0256F21 F, genomic survey sequence.
                                                                                                                                                                                                                                                                                              /lab_host="E. Coli strain XLIO-Gold, T1-resistant, F-"
/clone llb="Mouse 10kb plasmid UNGCNM library"
/note="Vector: PWD47xy, Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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Pred. No. 1.7e+07;
0; Mismatches 3.
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0224 row: O column: 19
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
                                                                                                                                                 organism="Mus musculus"
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Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                           /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                       High quality sequence stop: 19.
Location/Qualifiers
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                                                                                                                                                                                                                                                clone="UUGC1M0224019"
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AZ454430.1 GI:10612555
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76.9%;
                                                                                                                                                                                                                                                                            sex="Male"
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Best Local Similarity 76.9
Matches 10; Conservative
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S Dun, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacres, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Diasmid inserts

Diasmid inserts

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
                                                                                                                                                                                                                                                                                                                                                                                                            (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMM22 (gi|4732114|gb|RF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into
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                                                                                                                                                                                                                                                                                              /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"/clone_lib="Mouse_lokb plasmid UTGCIM library."
/note="Wector: PWD4Zhry; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
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Pred. No. 1.7e+07;
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Insert Length: 10000 Std Error: 0.00
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                    Seg primer: CACACAGAAACACCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers
                                                                                                                                                    /organism="Mus musculus"
                                                                                                                                                                        /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                            'db xref="taxon:10090"
                                                                                                                                                                                                                                                   /clone="UUGC1M0188G18"
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                                                                                                                                                                                                                                                                            /sex="Male"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10; Conservative
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Fax: 801 585 7177
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Best Local Similarity
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/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/clone_lib="Wouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from he Jackson
Laboratory Mouse DNA Resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerses and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gfrom a derivative
of pwD42 (gi|4732114|gb|AR129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent B. coli X110-Gold (Stratagene) cells
and selected for ampicillin resistance."
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Insert Length: 10000 Std Error: 0.00
Plate: 0513 row: 0 column: 16
Seg primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                       /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
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Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                            /db_xref="taxon:10090"
/clone="UUGC1M0513016"
                                                      Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                            sex="Male
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Fax: 801 585 7177
Email: ddunn@qenet
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chttp://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwalp4 (gql 47321141gbl A7129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xii0-Gold (Stratagene) cells and selected for ampicillin resistance."
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 19)
1 (bases 1 to 19)
1 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
1slam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah Genome Center
University of Utah
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1M0513016R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGC1M0513016 R, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                 /lab_host="E. Coli strain XLIO-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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Insert Length: 10000 Std Error: 0.00
                           Seg primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers
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                                                                                                                                                                                                                                                                  'db_xref="taxon:10090"
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76.9%;
                                                                                                                                                                                                                                                                                                                               sex="Male"
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Best Local Similarity 76.9
Matches 10; Conservative
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Fax: 801 585 7177
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84112, USA
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(http://www.jax.org/resources/documents/dhares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pware (adaptore omplementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XLLO-Gold (Stratagene) cells and selected for ampicillin resistance."
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Arabidopsis thaliana T-DNA flanking sequence, left border, clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Brunaud, V., Balzergue, S., Dubreucq, B., Aubourg, S., Samson, F., Chauvin, S., Bechtold, N., Cruaud, C., DeRose, R., Pelletier, G., Lepiniec, L., Caboche, M. and Lecharny, A.

T-DNA integration into the Arabidopsis genome depends on sequences
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                                                                                                                                                                                                                                                                                                                                                    /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone llb="Mouse lOkb plasmid UNGCNM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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AJ594088
AJ594088.1 GI:37943712
GSS; left border; T-DNA flanking sequence.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Laboratory Mouse DNA Resource
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EMBO Rep. 3 (12), 1152-1157 (2002)
Plate: 0025 row: D column: 18
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 19.
                                                                                                                                                                              orqanism="Mus musculus"
                                                                                                                                                                                                          /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                    'db xref="taxon:10090"
                                                                                                                                                                                                                                                                                                clone="UUGC2M0025D18"
                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                               sex="Male"
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Balzergue, S.
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                                                                                                                                                                                                                                                                                                                                                 /lab hose="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/clone_lib="Wouse 10kb plasmid UUGCIM library"
/note="Vector: FWD4Znv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.05 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel.
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4712114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptores complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
E 1 (bases 1 to 19)
S Dum, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacze, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.,
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
University of Utah
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2M0025D18F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0025D18 F, genomic survey sequence.
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Pred. No. 1.7e+07;
0; Mismatches 3; Indels
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Insert Length: 10000 Std Error: 0.00
Plate: 0531 row: N column: 06
Seg primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers
                                                                                                                                                                              organism="Mus musculus"
                                                                                                                                                                                                             /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                 db_xref="taxon:10090"
/clone="UUGCIM0531N06"
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76.9%;
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Fax: 801 585 7177
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Unpublished (2003)
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KEYWORDS
SOURCE
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Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Genome Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
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Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T.,
Reilly, M., Rose, M., Rose, K., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Waiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
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1M0080H05R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0080H05 R, genomic survey sequence.
the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at http://dbsgap.versailles.inra.fr/publiclines/. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (http://www.genoplante.com and http://genoplante-infobiogen.fr).
                                                                                                                                                                                                                                                                                                                                                                /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
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0
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                                                                                                                                                                                                                                          /organism="Arabidopsis thaliana"
/mol type="genomic DNA"
/cultivar="Wassillewskija"
/db xref="taxon:3702"
/clone="392P11"

    .12
/note="T-DNA flanking sequence
left border"

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Fax: 801 585 7177
Email: ddunm@genetics.utah.edu
Insert Length: 10000 Std Brror: 0.00
Plate: 0080 row: H column: 05
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Seg primer: CACACAGGAAACAGCTATGACC
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/mol_type="genomic DNA"
/strain="C578L/6J"
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High quality sequence stop: 20.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 8; Conserv
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AZ345710
LOCUS
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch oritice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWADA2 (gilfa732114 [gb] AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CL423876 11-808 UniformMu MuTAIL Library Zea mays genomic clone 01S0750-04C1-D08, genomic survey sequence.
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/clone="0150750-04C1-D08"
/clone="1b="UniformWu MuTAIL Library"
/note="Vector: TOPO-PCR4; DNA flanking Mu transposon insertions in Mu inactive lines were extracted from the UniformMu maize population by the thermo assymmetric interlaced PCR (TAIL) protocol using primers specific for the Mu terminal inverted repeat and a set of 16 arbitrary primers. Amplicons were size enriched using Sepharose 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence Sequence flanking probable Mu insertion site in UniformMu line: 01S0750-04, Primer set: C Class: transposon insertion site. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD clade, Panicoldeae, Andropogoneae, Zea.
                          /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 14)
Latshaw,S., Tan,B-.C., Settles,A.M. and McCarty,D.R.
Sequence tagged transposon insertions from the UniformMu maize
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0
'clone lib="Mouse 10kb plasmid UUGC1M library"
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Plant Molecular and Cellular Biology Program
University of Florida
Pol 10690 Gainesville, FL 32611-0690, USA
Enel: 352-392-1928 x322
Email: drm@ufl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40.0%; Score 8; DB 8; Le 68.8%; Pred. No. 2.2e+07; iive 0; Mismatches 5;
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/mol type="genomic DNA"
/strain="W22 (ACR, bz1-m9)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'cultivar="UniformMu"
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Submitted (23-007-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Evry cedex, FRANCE
PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequence from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at http://dbsgap.versailles.inra.fr/publiclines/. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).
Arabidopsis thaliana
Arabidopsis thaliana
Bukaryota, Virtidiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                    Brunaud, V., Balzergue, S., Dubreucq, B., Aubourg, S., Samson, F., Chauvin, S., Bechtold, N., Cruaud, C., DeRose, R., Pelletier, G., Lepiniec, L., Caboche, M. and Lecharny, A.

T-DNA integration into the Arabidopsis genome depends on sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases I to 19)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Reilly, M., Rose, M., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von Miederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AZ355195 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0094G22 R, genomic survey sequence.
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/organism="Arabidopsis thaliana"
/organism="Washilowskija"
/cultivar="Wassillewskija"
/db_xref="taxon:3702"
/clone="312606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39.0%; Score 7.8; DB 9;
81.8%; Pred. No. 2.7e+07;
iive 0; Mismatches 2;
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note="T-DNA flanking sequence
                                                                                                                                                                                                                                   of pre-insertion sites
EMBO Rep. 3 (12), 1152-1157 (2002)
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AZ355195.1 GI:10467355
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Balzergue, S.
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Matches 9; Conserv
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AZ355195
LOCUS
                                                                                                                    REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                  PUBMED
REFERENCE
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: hickegg@cc.umanitoba.ca
U3NeoSV1 gene trap. Tag generated by plasmid rescue. Additional
sequence information and target gene cloning can be generated. BS
cell line harboring insertion mutation of target gene is available.
Sequence analysis available from
http://140.193.242.7/esdb/public_search_frame.php?PST=PST7640-NL.Se
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AA587709

Arabidopsis thaliana T-DNA flanking sequence, left border, clone 312606, genomic survey sequence.

AJ587709

AJ587709.1 GI:37937333

GSS; left border; T-DNA flanking sequence.
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                                                                                                                                                                                                                                                                                                                  CL438505 14 bp DNA linear GSS 18-MAR-2004 PST7640-NL.Seq MICBl Mus musculus genomic clone PST7640-NL.Seq similar to Eif4a2, genomic survey sequence.
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Mukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 14)
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                                                                                                                        Gaps
         spin columns and cloned into the TOPO PCR4 vector."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Hicks GG
Contact: Hicks GG
Mammalian Functional Genomics Centre
Manitoba Institute of Cell Biology, Universitry of Manitoba
707629, 675 McDermot Ave, Winnipeg, MB R3E 0V9, Canada
Tel: 204 787 2190
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                                                                          Length 14
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                                                                                                                      2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /cell_type="Embryonic stem cell"
|cell_line="D3H (J1 subclone)"
|clone lib="MICB1"
|note="Vector: U3NeoSV1"
                                                                     Score 7.8; DB 9;
Pred. No. 2.6e+07;
                                                                                                                    0; Mismatches
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/strain="129 sv"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:10090"
/clone="PST7640-NL.Seq"
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Class: Gene Trap.
Location/Qualifiers
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81.8%;
                                                                       39.0%;
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                                                   Query Match
Best Local Similarity 81.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               www.EScells.ca
Unpublished (2002)
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Best Local Similarity 81.6
Matches 9; Conservative
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JOURNAL
COMMENT
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AUTHORS
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AJ587709
LOCUS
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SOURCE
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KEYWORDS
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Gaps

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GSS 02-OCT-2000

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/sex="Male"
/lab host="B. Coli strain XL10-Gold, T1-resistant, F-"
/lab host="B. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                        Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
                                                                                                      Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0201 row: E column: 16
Seq primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                            organism="Mus musculus"
       University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                              /mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:10090"
/clone="UUGC1M0201E16"
                                                                                                                                                                                                                                                                                  High quality sequence stop: 19.
Location/Qualifiers
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AZ875430
LOCUS
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymuclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMDA2 (gri #742114|gp|AR12972.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xiii0-Gold (Stratagene) cells and selected for ampicillin resistance."
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.

1 (bases 1 to 19)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AZ422531
1M0201E16F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC1M0201E16 F, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone lib="Mouse 10kb plasmid UTGCIM library."
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
84112, USA
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Pred. No. 2.7e+07;
0; Mismatches 2; Indels
                                                                                                                                                              Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Laboratory Mouse DNA Resource
                                                                                                                                                                                                          Plate: 0094 row: G column: 22
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                            /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/67"
                                                                                                                                                                                                                                                                                                                                                                                                                                       /db xref="taxon:10090"
/clone="UUGC1M0094G22"
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81.8%;
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Best Local Similarity 81.00,
Best Local Similarity 61.00,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /sex="Male
                                                                                                              Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 ACCGCATAGAC 12
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligomucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gal electrophoresis. Vector DNA was prepared from a derivative of pMAP12012.1, a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XLLO-Gold (Stratagene) cells and selected for ampicillin resistance."
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2M0189K09R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC2M0189K09 R, genomic survey sequence.
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Dunn, D., Aoyaqi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Nielly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weise, R., Mouse, whole genome scaffolding with paired end reads from 10kb
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Mus musculus
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                 PUBMED
                                       REFERENCE
                                                                AUTHORS
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AJ599121
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Arabidopsis thaliana T-DNA flanking sequence, left border, clone 412H07, genomic survey sequence.

Au595189

Au595189.1 GI:37944813

GSS; left border; T-DNA flanking sequence.

Arabidopsis thaliana (thale cress)

Arabidopsis thaliana (thale cress)

Arabidopsis thaliana (thale cress)

Arabidopsis thaliana (sequence.)

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T-DNA integration into the Arabidopsis genome depends on sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse_lokb plasmid UDGCIM library"
/note="Vector: PWD4Zly; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
84112, USA
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                                                                                                                                                          Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0189 row: K column: 09
Seg primer: CACACAGGAAACAGCTAATGACC
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EMBO Rep. 3 (12), 1152-1157 (2002)
22363535
                                                                                                                                                                                                                                                                                                                                                        /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                    Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:10090"
/clone="UUGC2M0189K09"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 81.6
                                                                                                             Tel: 801 585 5606
Fax: 801 585 7177
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Balzergue, S.

Balzergue, S.

Direct Submission

Submitted (13-0CT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue

Submitted (23-0CT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue

Gaston Cremieux, 91057 Bry cedex, FRANCE

PCR was performed on DNA from transformants of Arabidopsis thaliana

plants from INRA (Versailles). The DNA fragment(s) resulting from

the PCR were directly sequence flanking the insertion. T-DNA

derived sequences were removed. Information to order the

corresponding mutant line and a link to a database providing a

graphical display of the insertion site are available at

http://dbsgap.versailles.inra.fr/publiclines/. This sequence has

program Generated in the framework of the French plant genomics

program Generated info.info.infosiogen.fr).

Location/Qualifiers
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Arabidopsis thaliana T-DNA flanking sequence, left border, clone
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GSS, left border; T-DNA flanking sequence.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Bukariota; Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; crosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G.,
Lepiniec,L., Caboche,M. and Lecharny,A.
T-DNA integration into the Arabidopais genome depends on sequences
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/organism="Arabidopsis thaliana"
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81.8%; Pred. No. 2.7e+07;
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EMBO Rep. 3 (12), 1152-1157 (2002)
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Balzergue, S.
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PRI0137a_F08_2 - PRI0137a_BR (19) Mixed stage fosmid library of P. pacificus var. California Pristionchus pacificus genomic, genomic survey sequence.
CL683526
CL683526.1 GI:50191279
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http://dbsgap.versailles.inra.fr/publiclines/. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (http://www.genoplante.com and http://genoplante-info.info.biogen.fr).

Location/Qualifiers
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Pristionchus pacificus
Bukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Bukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Budoiplogasteridae; Pristionchus.

1 (bases 1 to 19)
Srinivasan, J., Otto, G.W., Kahlow, U., Geisler, R. and Sommer, R.J.
Srinivasan, J., Otto, G.W., Kahlow, U., Geisler, R. and Sommer, R.J.
Pristionchus pacificus
Nucleic Acids Res.
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Contact: Sommer RJ
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81.8%; Pred. No. 2.7e+07;
tive 0; Mismatches 2; Indels
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Pred. No. 2.7e+07;
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left border"
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THIS PROFES BILLIAM